

**FIGURE 8**

GCCCCGCGCCCCGGCGCCGGGCGCCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGA  
GCCTGCTCCCTGCTCAGCTGCGCGTCCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAG  
CTGCTGCCCCGCCAGCCGCAACTCCACCGTGAGCCGCTCATCTTCACGTTCTTCCTCTTCC  
TGGGGGTGCTGGTGTCCATCATTATGCTGAGCCCCGGGCGTGGAGAGTCAGCTCTACAAGCTG  
CCCTGGGTGTGTGAGGAGGGGGCCGGGATCCCCACCGTCCTGCAGGGCCACATCGACTGTGG  
CTCCCTGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCCTTCTTCTTCT  
TCTTTTTTCAACCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAG  
AATGGGTTTTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCCTCACCGTGGGTGCCTTCTACAT  
CCCTGACGGCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCGTGGGCTCCTTCCTCTTCA  
TCCTCATCCAGCTGGTGCTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGTGGCTGGGC  
AAGGCCGAGGAGTGCGATTCCCGTGCTGGTACGCAGGCCTCTTCTTCTTCACTCTCCTCTT  
CTACTTGCTGTGATCGCGGCGGTGGCGCTGATGTTTATGTACTACACTGAGCCCAGCGGCT  
GCCACGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCT  
GCTGTCTGCCCCAAGGTCCAGGACGCCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTCTAT  
CACCTCTACACCATGTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCA  
ACCCCCATTTGCCAACCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAG  
ACCCAGTGGTGGGATGCCCCGAGCATTGTGGGCCTCATCATCTTCCTCCTGTGCACCCTCTT  
CATCAGTCTGCGCTCCTCAGACCACCGGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCC  
CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGCAGGTGGCAGCCTGTGAGGGCCGGGCC  
TTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCCTGGTGCT  
GGCCTCACTGCACGTATGATGACGCTCACCAACTGGTACAAGCCCCGGTGAGACCCGGAAGA  
TGATCAGCACGTGGACCGCCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTC  
TACCTGTGGACCCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTGAGGCAGCCT  
CACAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCT  
GCCCCCTCCCCACACCAATCAGCCAGGCTGAGCCCCCACCCTGCCCCAGCTCCAGGACCTG  
CCCCTGAGCCGGGCCTTCTAGTCGTAGTGCCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCA  
GAGCCCCATCCCCCGCCACACCCACACGGTGGAGCTGCCTCTTCTTCCCCCTCCTCCCTGT  
TGCCCATACTCAGCATCTCGGATGAAAGGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGG  
CTGCTGGAGAGAGCGGGGAACTCCCACCACAGTGGGGCATCCGGCACTGAAGCCCTGGTGT  
CCTGGTCACGTCCCCCAGGGGACCCTGCCCCCTTCTTGGACTTCGTGCCTTACTGAGTCTCT  
AAGACTTTTTCTAATAACAAGCCAGTGCGTGTAACAAAAA

**FIGURE 9**

MGACLGACSLSCASCLCGSAPCILCSCCPASRNSTVSRLIFTFFLFLGVLSIIMLSPGVE  
SOLYKLPWVCEEAGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFTLLMLCVSSSRD  
PRAAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSFLFILIQLVLLIDFAHSW  
NQRWLGKAEECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFI SLNLTFC  
VCVSIAAVLPKVQDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVA  
GPEGYETQWWDAPSIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVA  
ACEGRAFDNEQDGVTSYSFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVWVKICAS  
WAGLLLYLWTLVAPLLLRNRDFS

**FIGURE 10**

GAGCGAGGCCGGGGACTGAAGGTGTGGGTGTGAGCCCTCTGGCAGAGGGTTAACCTGGGTC  
AAATGCACGGATTCTCACCTCGTACAGTTACGCTCTCCCGCGGCACGTCCGCGAGGACTTGA  
AGTCCTGAGCGCTCAAGTTTGTCCGTAGGTGAGAGAAAGGCCATGGAGGTGCCGCCACCGGC  
ACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCTATTTCCCCGAGTCTTTGCTGCCGAAGCTG  
TGACTGCCGATTCCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCC  
TATTACCCGGAATCTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAG  
AATTTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGG  
TGTATGGGGGAATACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCA  
GAAATTTATCATAACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTT  
CATTGCTTATGGCTGGCGCTGGGGTTGGAGAACTGCAGTGTTTGTGACTATATTCAACACAG  
TGAACACTAGTCTGAATGTATACCGAAATAAGATGCCTTAAGCCATTTTGTAATTGCAGGA  
GCTGTCACGGGAAGTCTTTTTTAGGATAAACGTAGGCCTGCGTGGCCTGGTGGCTGGTGGCAT  
AATTGGAGCCTTGCTGGGCACTCCTGTAGGAGGCCTGCTGATGGCATTTCAGAAGTACGCTG  
GTGAGACTGTTTCAGGAAAGAAAACAGAAGGATCGAAAGGCACTCCATGAGCTAAAACCTGGAA  
GAGTGGAAGGCAGACTACAAGTTACTGAGCACCTCCCTGAGAAAATTGAAAGTAGTTTACG  
GGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCTAAACCTTCCTAGAAACC  
CTTCAGTAATAGATAAACAAGACAAGGACTGAAAGTGCTCTGAACTTGAAACTCACTGGAGA  
GCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGC  
TGACAAATTTAAGTGCTGGTACCTGTGGTGGCAGTGGCTTGCTCTTGTCTTTTTCTTTTCTT  
TTTAACTAAGAATGGGGCTGTTGTACTCTCACTTTACTTATCCTTAAATTTAAATACATACT  
TATGTTTGTATTAATCTATCAATATATGCATACATGGATATATCCACCCACCTAGATTTTAA  
GCAGTAAATAAAACATTTTCGCAAAAGATTAAAGTTGAATTTTACAGTTT

**FIGURE 11**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318  
><subunit 1 of 1, 285 aa, 1 stop  
><MW: 32190, pI: 9.03, NX(S/T): 2  
MEVPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRRLRELF  
GKDEQQRISKDLANICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAIEYHNRFDAVQSAH  
RAATRGFIRYGWRGWRTAVFVTIFNTVNTSLNVYRNKDALSHFVIAGAVTGSLFRINVGLR  
GLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDRKALHELKLEEWKGRLQVTEHLPE  
KIESSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD

**Important Features:****Signal Peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 76-96 and amino acids 171-195

**N-glycosylation site:**

amino acids 153-156

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**FIGURE 12**

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA  
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGGA  
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAA  
TACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCAT  
AACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTCGTTTCATG  
GCTGGCGCCGAACC

**FIGURE 13**

TCAAGTTTGTCCGTAGGTGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTT  
TTTTCTGTAGAGCATTGTGCCTATTTCCCCGAGTTTTTGCTGCCGAAGCTGTGACTGCCGAT  
TCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA  
ATTTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGG  
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGA  
ATACCAGCTTTTATTCATGNTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATNA  
TAACC

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**FIGURE 15**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979  
><subunit 1 of 1, 204 aa, 1 stop  
><MW: 22147, pI: 8.37, NX(S/T): 3  
MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVIIVGIFLFLIALV  
GLIGAVKHHQVLLFFYMIILLLVFIVQFSVSCACLALNQEQQGOLLEVGNNTASARNDIQR  
NLNCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRFRVGGIGLFFSFTEILGVWL  
TYRYRNQKDPANPSAFL

**Signal Peptide:**

amino acids 1-34

**Transmembrane domains:**

amino acids 47-63, 72-95 and 162-182

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**FIGURE 16**

TGATTGGAGCTGTAAAAAANTCTTCAGGTGTTGTNATTTTTTTATATGATTATTCTGTAANT  
TGTATTTATTGTTTCAGTTTTNTGTATCTTGCGCTTGTTTAGCCNTGAACCAGGAGCAACAGG  
GTCAGNTTNTGGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT  
NTAAACTGCTGTGGGTTCCGAAGTGTTAACCCTGACACCTGTNTGGCTAGCTGTGTTAA  
AAGTGACCACTNGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGA  
GATTTGTTGGTGGCATTGGCCTGTTNTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACC  
TACAGATACAGGAACCAG

FIGURE 17

AATCCCAAATTCCCCAATTTTTTTGGNCTTTTATAGGGAAAGATGTGTTGTGGTAAAAAGTGT  
TAGTATAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAATAG  
TTATGTCCTTAGGAAATTGTGGTTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTG  
GTTTCATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCCATCAGAATGGAACG  
AGTTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTTATATAATTTGAAG  
TCTAAAAGACTGCATTTTTTAAACAAGTTAGTATTAATGCGTTGGCCCACGTAGCAAAAAGAT  
ATTTGATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAAGTTCTCAGTATTGTAACAGC  
AACTTGTCAAACCTAAGCATATTTGAATATGATCTCCCATAAATTTGAAATTGAAATCGTATT  
GTGTGGAGGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC  
CCTTGC

**FIGURE 18**

ATGATTATTCTGTTACTTGTATTTATTGTTTCAGTTTATGGTATCTTGCGCTTGTTTAGCCC  
CTGAAACCAGGAGCAACAGGGNNCAGCTTCCTGGAGGTTGGTTGGCAACAATCACGGCCAAG  
TGACTCCGCAAATGACATCCCAGAGAAATCCTAAACTGCTGTGGGTTCCGAAGTGTTAACCC  
AAATGACACCTGTCTGGCTNGCTGTGTTAAAAGTGACCACTCGTGCTCGCCATGTGCTCCAA  
TCATAGGAGAATATGC

**FIGURE 19**

CAGTCACCATGAAGCTGGGCTGTGTCCTCATGGCCTGGGCCCTCTACCTTTCCTTGGTGTG  
CTCTGGGTGGCCCAGATGCTACTGGCTGCCAGTTTTGAGACGCTGCAGTGTGAGGGACCTGT  
CTGCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCT  
TCCAGGTCAAGGCCTACACTTTCAGTGAACCTTCCACCTGATTGTGTCTATGACTGGCTG  
ATCCTCCAAGGTCCAGCCAAGCCAGTTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGC  
CTGGCAAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCC  
CCGGGCCTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCAC  
TGCAGTGGCATCTTCCAGAGCCCTGGTCCTGGGATCCCAGAAACAGCATCTGTTGTGGCTAT  
CACAGTCCAAGAACTGTTTCCAGCGCCAATTCTCAGAGCTGTACCCTCAGCTGAACCCCAAG  
CAGGAAGCCCCATGACCCTGAGTTGTCAGACAAAGTTGCCCCCTGCAGAGGTGAGCTGCCCCG  
CTCCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATT  
CCAGATCCCCACAGCTTCAGAAGATCACTCCGGGTCATACTGGTGTGAGGCAGCCACTGAGG  
ACAACCAAGTTTGGAAACAGAGCCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCT  
GCTGCACCTCCCACATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAAGTCTCCTGA  
GGAGGCCCTGGGCTCTGCCTCCGCCGCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTT  
CTCCTCTGGGGATGCCAGATCCTCATCTGTATCACCAGATGGGCCTTCTTCTCAAACACATG  
CAGGATGTGAGAGTCCTCCTCGGTCACCTGCTCATGGAGTTGAGGGAATTATCTGGCCACCA  
GAAGCCTGGGACCACAAAGGCTACTGCTGAATAGAAAGTAAACAGTTTCATCCATGATCTCACT  
TAACCACCCCAATAAATCTGATTCTTTATTTTCTTCTCCTGTCTGACATATGCATAAGTA  
CTTTTACAAGTTGTCCCAGTGTTTTGTAGAAATAATGTAGTTAGGTGAGTGTAATAAATTT  
ATATAAAGTGAGAATTAGAGTTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTC  
TGCTGTCTAGATCAGGAATTTCTATCTGTTATATCGACCAGAATGTTGTGATTTAAAGAGAA  
CTAATGGAAGTGGATTGAATACAGCAGTCTCAACTGGGGGCAATTTTGCCCCCAGAGGACA  
TTGGGCAATGTTTGGAGACATTTTGGTCATTATACTTGGGGGGTGGGGGATGGTGGGATGT  
GTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAAACATCCTATAATGCACAG  
GGCAGTACCCCAACAACGAAAAATAATCTGGCCCAAATGTCAGTTGTACTGAGTTTGAGAAA  
CCCCAGCCTAATGAAACCCTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTAT  
TATCTCTTTCCAGCCTCATTGAGCTATTCTTACTGACATAACCAGTCTTTAGCTGGTGCTATG  
GTCTGTTCTTTAGTTCTAGTTTGTATCCCCTCAAAGCCATTATGTTGAAATCCTAATCCCC  
AAGGTGATGGCATTAAAGAAGTGGGCCTTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC  
ATGATTAGGATTAGTGCCCTTATTTAAAAAGGCCCCAGAGAGCTAACTCACCTTCCACCAT  
ATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCACAAAAACAGCTGTCCCAAACACCG  
ACTCTGTCGTTGCCTTGATCTTGAACCTCCAGCCTCCAGAACTATGAGAAATAAATTTCTGG  
TTGTTTGTAGCCTAA



**FIGURE 20**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594  
><subunit 1 of 1, 359 aa, 1 stop  
><MW: 38899, pI: 5.21, NX(S/T): 0  
MKLGCVLMAWALYLSLGVLWVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQV  
KAYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRQAWQDWPLTQVTFYRDGSALGPPGP  
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGS  
PMTLSCQTKLPLQRSAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ  
VWKQSPQLEIRVQGASSSAAPPTLNPAPQKSAAPGTAPEEAPGPLPPPPTPSSSEDPGFSSPL  
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

Leucine zipper pattern sequence:

amino acids 12-33

Protein kinase C phosphorylation site:

amino acids 353-355

**FIGURE 21**

CCCACGCGTCCGCCCCACGCGTCCGCCCCACGGGTCCGCCCCACGCGTCCGGGCCACCAGAAGTT  
TGAGCCTCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAGTAGCTCTGGCTGTGATGGGG  
ATCTTACTGGGCCTGCTACTCCTGGGGCACCTAACAGTGGACACTTATGGCCGTCCCATCCT  
GGAAGTGCCAGAGAGTGTAACAGGACCTTGGAAAGGGGATGTGAATCTTCCCTGCACCTATG  
ACCCCTGCAAGGCTACACCCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCCT  
GTCACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAAGTACCAGGGCCG  
CCTGCATGTGAGCCACAAGGTTCCAGGAGATGTATCCCTCCAATTGAGCACCTGGAGATGG  
ATGACCGGAGCCACTACACGTGTGAAGTCACCTGGCAGACTCCTGATGGCAACCAAGTCGTG  
AGAGATAAGATTACTGAGCTCCGTGTCCAGAACTCTCTGTCTCCAAGCCCACAGTGACAAC  
TGGCAGCGGTTATGGCTTCACGGTGCCCCAGGGAATGAGGATTAGCCTTCAATGCCAGGCTC  
GGGGTTCTCCTCCCATCAGTTATATTTGGTATAAGCAACAGACTAATAACCAGGAACCCATC  
AAAGTAGCAACCCTAAGTACCTTACTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA  
TTTCTGCACTGCCAAGGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTGTGAAGTTTGTGG  
TCAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC  
TTGAAAGCAACATCTACAGTGAAGCAGTCCTGGGACTGGACCACTGACATGGATGGCTACCT  
TGGAGAGACCAGTGCTGGGCCAGGAAAGAGCCTGCCTGTCTTTGCCATCATCCTCATCATCT  
CCTTGTGCTGTATGGTGGTTTTTACCATGGCCTATATCATGCTCTGTGCGAAGACATCCCAA  
CAAGAGCATGTCTACGAAGCAGCCAGGTAAGAAAGTCTCTCCTCTTCCATTTTTTGACCCCGT  
CCCTGCCCTCAATTTTTGATTACTGGCAGGAAATGTGGAGGAAGGGGGGTGTGGCACAGACCC  
AATCCTAAGGCCGGAGGCCTTCAGGGTCAGGACATAGCTGCCTTCCCTCTCTCAGGCACCTT  
CTGAGGTTGTTTTGGCCCTCTGAACACAAAGGATAATTTAGATCCATCTGCCTTCTGCTTCC  
AGAATCCCTGGGTGGTAGGATCCTGATAATTAATTGGCAAGAATTGAGGCAGAAGGGTGGGA  
AACCAGGACCACAGCCCCAAGTCCCTTCTTATGGGTGGTGGGCTCTTGGGCCATAGGGCACA  
TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGGTGGCCATCTTCGCAAGTGGCTGCT  
CCAGTGATGAGCCAACCTTCCCAGAATCTGGGCAACAACACTACTCTGATGAGCCCTGCATAGGA  
CAGGAGTACCAGATCATCGCCAGATCAATGGCAACTACGCCCCGCTGCTGGACACAGTTCC  
TCTGGATTATGAGTTTCTGGCCACTGAGGGCAAAAGTGTCTGTAAAAATGCCCCATTAGGC  
CAGGATCTGCTGACATAATTGCCTAGTCAGTCCTTGCCTTCTGCATGGCCTTCTTCCCTGCT  
ACCTCTCTTCCCTGGATAGCCCAAAGTGTCCGCCTACCAACACTGGAGCCGCTGGGAGTCACT  
GGCTTTGCCCTGGAATTTGCCAGATGCATCTCAAGTAAGCCAGCTGCTGGATTTGGCTCTGG  
GCCCTTCTAGTATCTCTGCCGGGGGCTTCTGGTACTCCTCTCTAAATACCAGAGGGAAGATG  
CCCATAGCACTAGGACTTGGTCATCATGCCTACAGACACTATTCAACTTTGGCATCTTGCCA  
CCAGAAGACCCGAGGGAGGCTCAGCTCTGCCAGCTCAGAGGACCAGCTATATCCAGGATCAT  
TTCTCTTTCTTCAGGGCCAGACAGCTTTTAATTGAAATTGTTATTTACAGGCCAGGGTTCA  
GTTCTGCTCCTCCACTATAAGTCTAATGTTCTGACTCTCTCCTGGTGCTCAATAAATATCTA  
ATCATAACAGC

**FIGURE 22**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416  
><subunit 1 of 1, 321 aa, 1 stop  
><MW: 35544, pI: 8.51, NX(S/T): 0  
MGILLGLLLLLGHLLTVDTYGRPILEVPESVTGPWKGDVNLPCITYDPLQGYTQVLVKWLVRGS  
DPVTIFLRDSSGDHIQQAKYQGRLVSHKVPDVSLLQLSTLEMDDRSHYTCEVTWQTPDGNQ  
VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRLSLQCQARGSPPISYIWKQQTNNQE  
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKTEAPTMT  
YPLKATSTVKQSWDWTDDMDGYLGETSAGPGKSLPVFAIILIIISLCCMVVFTMAYIMLCRKT  
SQQEHVYEAAAR

Glycosaminoglycan attachment site:

amino acids 149-152

Transmembrane domain:

amino acids 276-306

**FIGURE 23**

GCGCCGGGAGCCCATCTGCCCCCAGGGGCACGGGGCGCGGGGCGGGCTCCCGCCCGGCACAT  
GGCTGCAGCCACCTCGCGCGCACCCCGAGGGCGCGCGCCAGCTCGCCCGAGGTCCGTCCGA  
GGCGCCCGGGCCCGCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATC  
GGGATGTCCTCCTCCTTCTCCTCTTGCTAGTTTCCTACTATGTTGGAACCTTGGGGACTCA  
CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACCTTTGCCCTGCCACCATCAACTGGGGC  
TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAAA  
GTGGTGATCACTTACTCCAGTCGTCTGTCTACAATACTTGACTGAGGAACAGAAGGGCCG  
AGTGGCCTTTGCTTCCAATTTCTTGCGAGGAGATGCCTCCTTGCGAGATTGAACCTCTGAAGC  
CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTCAGGGCGCTACGTGTGGAGCCAT  
GTCATCTTAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC  
AGAAGGAAGTGACCTGACTTTGCGAGTGTGAGTCATCCTCTGGCACAGAGCCCATTTGTGTATT  
ACTGGCAGCGAATCCGAGAGAAAGAGGGGAGAGGATGAACGTCTGCCTCCCAAATCTAGGATT  
GACTACAACCACCTTGACGAGTTCTGCTGCAGAATCTTACCATGTCCTACTCTGGACTGTA  
CCAGTGACACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAACTGTACAGT  
ATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG  
ATTTTCCTCTTGCTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA  
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCT  
CCTCTTCCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCTCCTCCACTCGCTCCACAGCAAAT  
AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCAC  
CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATG  
CTAATCTGACCAAAGCAGAAACCACACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAA  
ACGGTCTGAATTACAATGGACTTGACTCCCACGCTTTCCTAGGAGTCAGGGTCTTTGGACTC  
TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA  
GTGAGCATTGCACGGAACAGATTGAGATGAGCATTTCCTTATACAATAACCAAACAAGCAA  
AGGATGTAAGCTGATTCATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG  
AAAGCAGGAGTCCAAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG  
AGGTGAATATACCTAAAACTTTTAAATGTGGGATATTTTGTATCAGTGCTTTGATTCACAATT  
TTCAAGAGGAAATGGGATGCTGTTTGTAAATTTTCTATGCATTTCTGCAAACCTTATTGGATT  
ATTAGTTATTGAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC  
TGAGCTAACCCTTCTAAGAAACTCCAAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC  
TTCATTTGTGATAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA  
AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTTGTATTGAGCCCAAATAAC  
TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTCATGATGTT  
ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCCTCAAAT  
CAGATGCCTCTAAGGACTTTCCTGCTAGATATTTCTGGAAGGAGAAAATACAACATGTGATT  
TATCAACGTCCTTAGAAAGAATTCTTCTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATTA  
CCCAACATACCATTTATAGTCTCTTCTTTCTGAGAAAATGTGAAACCAGAATTGCAAGACTGG  
GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA  
TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC  
ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

**FIGURE 24**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41281, pI: 8.33, NX(S/T): 3
MSLLLLLLLLVSYYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSSGSRSSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV
```

Transmembrane domain:

amino acids 221-254



**FIGURE 25**

GTCTGTTCTTTGCTCTCTCGCGCCAGTCCTCCTCCCTGGTTCTCCTCAGCCGCTGTCTGGAG  
GAGAGCACCCGGAGACGCGGGCTGCAGTCGCGGGCGGCTTCTCCCCGCTGGGCGGCCTCGCC  
GCTGGGCAGGTGCTGAGCGCCCCCTAGAGCCTCCCTTGCCGCTCCCTCCTCTGCCCCGGCCGC  
AGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGGCCCGGGAGGCGGCGGTGGATGC  
GGCGCTGGGCAGAAAGCAGCCGCGGATTCCAGCTGCCCCGCGCGCCCCGGGCGCCCCCTGCGAG  
TCCCCGGTTTCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGCCCTCGCCTCCTGCAGCCGC  
ATCGCCCCGCGGAGCCACAGCCACGATGATCGCGGGCTCCCTTCTCCTGCTTGGATTCTTTAG  
CACCACCACAGCTCAGCCAGAACAGAAGGCCTCGAATCTCATTGGCACATACCGCCATGTTG  
ACCGTGCCACCGGCCAGGTGCTAACCTGTGACAAGTGTCCAGCAGGAACCTATGTCTCTGAG  
CATTGTACCAACACAAGCCTGCGCGTCTGCAGCAGTTGCCCTGTGGGGACCTTTACCAGGCA  
TGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAATGATTGAGA  
AATTACCTTGTGCTGCCTTGACTGACCGAGAATGCACTTGCCACCTGGCATGTTCCAGTCT  
AACGCTACCTGTGCCCCCATAACGGTGTGTCTGTGGGTGGGGTGTGCGGAAGAAAGGGAC  
AGAGACTGAGGATGTGCGGTGTAAGCAGTGTGCTCGGGGTACCTTCTCAGATGTGCCTTCTA  
GTGTGATGAAATGCAAAGCATAACAGACTGTCTGAGTCAGAACCTGGTGGTGATCAAGCCG  
GGGACCAAGGAGACAGACAACGTCTGTGGCACACTCCCGTCTTCTCCAGCTCCACCTCACC  
TTCCCCCTGGCACAGCCATCTTTCCACGCCCTGAGCACATGGAAACCCATGAAGTCCCTTCT  
CCACTTATGTTCCCAAAGGCATGAACTCAACAGAATCCAACCTTCTGCTCTGTTAGACCA  
AAGGTACTGAGTAGCATCCAGGAAGGGACAGTCCCTGACAACACAAGCTCAGCAAGGGGGAA  
GGAAGACGTGAACAAGACCCTCCCAAACCTTCAGGTAGTCAACCACCAGCAAGGCCCCACC  
ACAGACACATCCTGAAGCTGCTGCCGTCCATGGAGGCCACTGGGGGCGAGAAGTCCAGCACG  
CCCATCAAGGGCCCCAAGAGGGGACATCCTAGACAGAACCTACACAAGCATTTTGACATCAA  
TGAGCATTTGCCCTGGATGATTGTGCTTTTCTGCTGCTGGTGCTTGTGGTGATTGTGGTGT  
GCAGTATCCGGAAAAGCTCGAGGACTCTGAAAAAGGGGCCCGGCAGGATCCCAGTGCCATT  
GTGGAAAAGGCAGGGCTGAAGAAATCCATGACTCCAACCCAGAACCAGGAGAAATGGATCTA  
CTACTGCAATGGCCATGGTATCGATATCCTGAAGCTTGTAGCAGCCCAAGTGGGAAGCCAGT  
GGAAAGATATCTATCAGTTTCTTTGCAATGCCAGTGAGAGGGAGGTTGCTGCTTTCTCCAAT  
GGGTACACAGCCGACCACGAGCGGGCCTACGCAGCTCTGCAGCACTGGACCATCCGGGGCCC  
CGAGGCCAGCCTCGCCCAGCTAATTAGCGCCCTGCGCCAGCACCGGAGAAACGATGTTGTGG  
AGAAGATTCTGTTGGGCTGATGGAAGACACCACCCAGCTGGAACTGACAACTAGCTCTCCCG  
ATGAGCCCCAGCCCGCTTAGCCCGAGCCCCATCCCCAGCCCCAACGCGAACTTGAGAATTC  
CGCTCTCCTGACGGTGGAGCCTTCCCCACAGGACAAGAACAAGGGCTTCTTCGTGGATGAGT  
CGGAGCCCCCTTCTCCGCTGTGACTCTACATCCAGCGGCTCCTCCGCGCTGAGCAGGAACGGT  
TCCTTTATTACCAAAGAAAAGAAGGACACAGTGTGCGGCAGGTACGCCTGGACCCCTGTGA  
CTTGCAGCCTATCTTTGATGACATGCTCCACTTTCTAAATCCTGAGGAGCTGCGGGTGATTG  
AAGAGATTCCCCAGGCTGAGGACAACTAGACCGGCTATTTCGAAATTATTGGAGTCAAGAGC  
CAGGAAGCCAGCCAGACCCTCCTGGACTCTGTTTATAGCCATCTTCCTGACCTGCTGTAGAA  
CATAGGGATACTGCATTCTGGAAATTACTCAATTTAGTGGCAGGGTGGTTTTTTAATTTCT  
TCTGTTTCTGATTTTTTGTGTTTGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT  
GTGTGTGTGTGTGTTTAAACAGAGAATATGGCCAGTGCTTGAGTTCTTTCTCCTTCTCTCTCT  
CTCTTTTTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTATAAGCCTTTGCCAGGTGTAAT  
GTTGTGAAATACCCACCCTAAAGTTTTTTAAGTTCCATATTTTCTCCATTTTGCCTTCTTA  
TGTATTTTCAAGATTATTCTGTGCACTTTAAATTTACTTAACTTACCATAAATGCAGTGTGA  
CTTTTCCACACACTGGATTGTGAGGCTCTTAACTTCTTAAAGTATAATGGCATCTTGTGA  
ATCCTATAAGCAGTCTTTATGTCTCTTAACATTACACCTACTTTTTTAAAAACAAATATTAT  
TACTATTTTATTATTGTTTGTCTTTATAAATTTTCTTAAAGATTAAGAAAATTTAAGACC  
CCATTGAGTTACTGTAATGCAATTCAACTTTGAGTTATCTTTTAAATATGTCTTGTATAGTT  
CATATTCATGGCTGAACTTGACCACACTATTGCTGATTGTATGGTTTTTACCTGGACACCG  
TGTAGAATGCTTGATTACTTGTACTCTTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAA  
ATCCTCAAGCCATCAGGATTTGCTATTTAAGTGGCTTGACAACCTGGGCCACCAAAGAACTTG  
AACTTCACCTTTTAGGATTTGAGCTGTTCTGGAACACATTGCTGCACTTTGGAAAGTCAAAA  
TCAAGTGCCAGTGGCGCCCTTTCCATAGAGAATTTGCCAGCTTTGCTTTAAAGATGTCTT  
GTTTTTTATATACACATAATCAATAGGTCCAATCTGCTCTCAAGGCCTTGGTCCTGGTGGGA  
TTCCTTCACCAATTACTTTAATTAAAAATGGCTGCAACTGTAAGAACCCTTGTCTGATATAT  
TTGCAACTATGCTCCCATTTACAAATGTACCTTCTAATGCTCAGTTGCCAGGTTCCAATGCA  
AAGGTGGCGTGGACTCCCTTTGTGTGGGTGGGGTTTTGTGGGTAGTGGTGAAGGACCGATATC  
AGAAAAATGCCTTCAAGTGTACTAATTTATTAATAAACATTAGGTGTTTGTAAAAAAAAA

**FIGURE 26**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594  
><subunit 1 of 1, 655 aa, 1 stop  
><MW: 71845, pI: 8.22, NX(S/T): 8  
MGTSPSSSTALASCSRIARRATATMIAGSLLLLGFLSTTTAQPEQKASNLIQTYRHVDRATG  
QVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQPCPWPMIEKLPCA  
ALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKKGTETEDVRCKQCARGTFSDVPSSVMKC  
KAYTDCLSQNLVVIKPGTKETDNVCGTLPSFSSSTSPSPGTAFPRPEHMETHEVPSSTYVP  
KGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVNVHQQGPVHRRHIL  
KLLPSMEATGGEKSSTPIKGPKRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVIVVCSIRK  
SSRTLKKGPRQDPSAIVEKAGLKKSMPTPTQNRKWIYYCNGHGDILKLVAQVGSQWKDIY  
QFLCNASEREVAAFSNGYTADHERAYAALQHWITRGPEASLAQLISALRQHRNDVVEKIRG  
LMEDTTQLETDKLALPMSPSPSPSPSPNAKLENSALLTVEPSPQDKNKGFFVDESEPLL  
RCDSTSSGSSALSRNGSFITKEKKDVLRLQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQ  
AEDKLDRLFETIGVKSQEASQTLLDSVYSHLPDLL

**FIGURE 27**

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCCGTGGTGCCATCTACATTTTTTGGGA  
CTCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCTTGAAATAGTCAC  
CATGGGGGAAAATGATCCGCCTGCTGTTGAAGCCCCCTTCTCATTCCGATCGCTTTTTTGGCC  
TTGATGATTTGAAAATAAGTCCTGTTGCACCAGATGCAGATGCTGTTGCTGCACAGATCCTG  
TCACTGCTGCCATTGAAGTTTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGC  
ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGGAAGTACAGATGTCGCTCATCCT  
TTAAGTGTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGAGGAC  
GAGTACCGCTGTGTCCGGGTGGGTGGTCAGAATGCCGTGCTCCAGGTGTTACAGCTGCTTC  
GTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAATGTTGCCTGTGCCCAAC  
TGGGTTTTCCCAAGCTATGTGAGTTCAGATAACCTCAGAGTGAGCTCGCTGGAGGGGCGAGTTC  
CGGGAGGAGTTTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCA  
CTCAGTATATGTGAGGGAGGGATGTGCCTCTGGCCACGTGGTTACCTTGCACTGCACAGCCT  
GTGGTCATAGAAGGGGCTACAGCTCACGCATCGTGGGTGGAAACATGTCCTTGCTCTCGCAG  
TGGCCCTGGCAGGCCAGCCTTCAGTTCCAGGGCTACCACCTGTGCGGGGGCTCTGTCTATCAC  
GCCCCTGTGGATCATCACTGCTGCACACTGTGTTTATGACTTGTACCTCCCCAAGTCATGGA  
CCATCCAGGTGGGTCTAGTTTCCCTGTTGGACAATCCAGCCCCATCCCACTTGGTGGAGAAG  
ATTGTCTACCACAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCT  
GGCCGGGCCACTCACGTTCAATGAAATGATCCAGCCTGTGTGCCTGCCCAACTCTGAAGAGA  
ACTTCCCCGATGGAAAAGTGTGCTGGACGTCAGGATGGGGGGCCACAGAGGATGGAGGTGAC  
GCCTCCCCTGTCTGAACCACGCGGCGCTCCCTTTGATTTCCAACAAGATCTGCAACCACAG  
GGACGTGTACGGTGGCATCATCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCG  
TGGACAGCTGCCAGGGGGACAGCGGGGGGGCCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAG  
TTAGTGGGAGCGACCAGCTTTGGCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGTGTACAC  
CCGTGTACCTCCTTCTGGACTGGATCCACGAGCAGATGGAGAGAGACCTAAAAACCTGAA  
GAGGAAGGGGACAAGTAGCCACCTGAGTTCCTGAGGTGATGAAGACAGCCCGATCCTCCCCT  
GGACTCCCGTGTAGGAACCTGCACACGAGCAGACACCCTTGAGAGCTCTGAGTTCCGGCACCA  
GTAGCAGGCCCCGAAAGAGGCACCCTTCCATCTGATTCCAGCACAACTTCAAGCTGCTTTTT  
GTTTTTTGTTTTTTTGAAGGTGGAGTCTCGCTCTGTTGCCAGGCTGGAGTGCAGTGGCGAAA  
TCCCTGCTCACTGCAGCCTCCGCTTCCCTGGTTCAAGCGATTCTCTTGCTCAGCTTCCCCA  
GTAGCTGGGACCACAGGTGCCCGCCACCACACCCAATAATTTTTGTATTTTTTAGTAGAGAC  
AGGGTTTACCATGTTGGCCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTGCCTGCTT  
CAGCCTCCCACAGTGCTGGGATTACAGGCATGGGCCACCACGCCTAGCCTCACGCTCCTTTC  
TGATCTTCACTAAGAACAAAAGAAGCAGCAACTTGCAAGGGCGGCCTTTCCCACTGGTCCAT  
CTGGTTTTCTCTCCAGGGTCTTGCAAAATTCTTGACGAGATAAGCAGTTATGTGACCTCAG  
TGCAAAGCCACCAACAGCCACTCAGAAAAGACGCACCAGCCCAGAAGTGCAGAACTGCAGTC  
ACTGCACGTTTTTCATCTCTAGGGACCAGAACCAACCCACCCTTTCTACTTCCAAGACTTAT  
TTTCACATGTGGGGAGGTTAATCTAGGAATGACTCGTTTAAGGCCTATTTTCATGATTTCTT  
TGTAGCATTTGGTGCTTGACGTATTATTGTCTTTGATTCCAAATAATATGTTTCCTTCCCT  
CATTGTCTGGCGTGTCTGCGTGGACTGGTGACGTGAATCAAATCATCCACTGAAA



**FIGURE 28**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234  
><subunit 1 of 1, 453 aa, 1 stop  
><MW: 49334, pI: 6.32, NX(S/T): 1  
MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALILA  
LAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVVRVGGQNAVLOVFTAAS  
WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIHLLPDDKVTALHH  
SVYVREGCASGHVVTLOCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVIT  
PLWIIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKL  
AGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAPPLISNKICNHR  
DVGIGIISPSMLCAGYLTGGVDSCQGDGGPLVCQERRLWKLVGATSFQIGCAEVNKPQVYT  
RVTSFLDWIHEQMERDLKT

**FIGURE 29**

CCCACGCGTCCGTCCCTAGTCCCCGGGCCAACTCGGACAGTTTGCTCATTTATTGCAACGGTC  
AAGGCTGGCTTGTGCCAGAACGGCGCGCGCGCGCACGCACGCACACACACGGGGGAAAC  
TTTTTTTAAAAATGAAAGGCTAGAAGAGCTCAGCGGCGGGCGGGCGCTGCGCGAGGGCTCCG  
GAGCTGACTCGCCGAGGCAGGAAATCCCTCCGGTCGCGACGCCCGGCCCGGCTCGGCGCCC  
GCGTGCGGATGGTGCAGCGCTCGCCGCCGGGGCCCGAGAGCTGCTGCACTGAAGGCCGGCGACG  
ATGGCAGCGCGCCCGCTGCCCGTGTCCCCCGCCCGCGCCCTCCTGCTCGCCCTGGCCGGTGC  
TCTGCTCGCGCCCTGCGAGGCCCGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAG  
TTGTCAGTGCCCTCTGTTCCGAGTGGGGACCTCTGGATCCCAGTGAAGAGCTTCGACTCCAAG  
AATCATCCAGAAGTGCTGAATATTCGACTACAACGGGAAAGCAAAGAACTGATCATAAATCT  
GGAAAGAAATGAAGGTCTCATTGCCAGCAGTTTCACGGAAACCCACTATCTGCAAGACGGTA  
CTGATGTCTCCCTCGCTCGAAATTACACGGGTCACTGTTACTACCATGGACATGTACGGGGA  
TATTCTGATTGAGCAGTCAGTCTCAGCACGTGTTCTGGTCTCAGGGGACTTATTGTGTTTGA  
AAATGAAAGCTATGTCTTAGAACCAATGAAAAGTGCAACCAACAGATACAAACTCTTCCCAG  
CGAAGAAGCTGAAAAGCGTCCGGGGATCATGTGGATCACATCACACACCAAACCTCGCT  
GCAAAGAATGTGTTTCCACCACCCTCTCAGACATGGGCAAGAAGGCATAAAAGAGAGACCCT  
CAAGGCAACTAAGTATGTGGAGCTGGTGATCGTGGCAGACAACCGAGAGTTTCAGAGGCAAG  
GAAAAGATCTGGAAAAAGTTAAGCAGCGATTAATAGAGATTGCTAATCACGTTGACAAGTTT  
TACAGACCACTGAACATTCCGATCGTGTTGGTAGGCGTGGAAGTGTGGAATGACATGGACAA  
ATGCTCTGTAAGTCAGGACCCATTACCAGCCTCCATGAATTTCTGGACTGGAGGAAGATGA  
AGCTTCTACCTCGCAAATCCCATGACAATGCGCAGCTTGTGAGTGGGGTTTATTTCCAAGGG  
ACCACCATCGGCATGGCCCCAATCATGAGCATGTGCACGGCAGACCAGTCTGGGGGAATTGT  
CATGGACCATTCAGACAATCCCCTTGGTGCAGCCGTGACCCTGGCACATGAGCTGGGCCACA  
ATTTCCGGGATGAATCATGACACACTGGACAGGGGCTGTAGCTGTCAAATGGCGGTTGAGAAA  
GGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCCATGGTGTTCAGCAGTTGCAG  
CAGGAAGGACTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTGTTTAACTGCCGG  
AAGTCAGGGAGTCTTTCCGGGGGCCAGAAGTGTGGGAACAGATTTGTGGAAGAAGGAGAGGAG  
TGTGACTGTGGGGAGCCAGAGGAATGTATGAATCGCTGCTGCAATGCCACCACCTGTACCCT  
GAAGCCGGACGCTGTGTGCGCACATGGGCTGTGCTGTGAAGACTGCCAGCTGAAGCCTGCAG  
GAACAGCGTGCAGGGACTCCAGCAACTCCTGTGACCTCCCAGAGTTCTGCACAGGGGCCAGC  
CCTCACTGCCCAGCCAATGTGTACCTGCACGATGGGCACTCATGTGAGGATGTGGACGGCTA  
CTGCTACAATGGCATCTGCCAGACTCACGAGCAGCAGTGTGTGACGCTCTGGGGACCAGGTG  
CTAAACCTGCCCCCTGGGATCTGCTTTGAGAGAGTCAATTCTGCAGGTGATCCTTATGGCAAC  
TGTGGCAAAGTCTCGAAGAGTTCTTTTGCCAAATGCGAGATGAGAGATGCTAAATGTGGA  
AATCCAGTGTCAAGGAGGTGCCAGCCGGCCAGTCATTGGTACCAATGCCGTTTCCATAGAAA  
CAAACATCCCTCTGCAGCAAGGAGGCGGATTCTGTGCCGGGGGACCCACGTGTACTTGGGC  
GATGACATGCCGGACCCAGGGCTTGTGCTTGCAGGCACAAAGTGTGCAGATGGAAAAATCTG  
CCTGAATCGTCAATGTCAAAATATTAGTGTCTTTGGGGTTTACGAGTGTGCAATGCAGTGCC  
ACGGCAGAGGGGTGTGCAACAACAGGAAGAACTGCCACTGCGAGGCCCCACTGGGCACCTCCC  
TTCTGTGACAAGTTTGGCTTTGGAGGAAGCACAGACAGCGGCCCATCCGGCAAGCAGAAGC  
AAGGCAGGAAGCTGCAGAGTCCAACAGGGAGCGCGGCCAGGGCCAGGAGCCCGTGGGATCGC  
AGGAGCATGCGTCTACTGCCTCACTGACACTCATCTGAGCCCTCCCATGACATGGAGACCGT  
GACCAGTGCTGCTGCAGAGGAGGTCACGCGTCCCCAAGGCCTCCTGTGACTGGCAGCATTGA  
CTCTGTGGCTTTGCCATCGTTTCCATGACAACAGACACAACACAGTTCTCGGGGCTCAGGAG  
GGGAAGTCCAGCCTACCAGGCACGTCTGCAGAAACAGTGCAAGGAAGGGCAGCGACTTCCTG  
GTTGAGCTTCTGCTAAACATGGACATGCTTCAGTGCTGCTCCTGAGAGAGTAGCAGGTTAC  
CACTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAGTCTGGCCTTTTAC  
TGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTTGGGCCCAGTGTCCCCTTTCCCAGTGA  
CACCTCAGCCTTGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGATATGGC  
TTTTAGCATTTATTATATGAAAATAGCAGGGTTTTAGTTTTTAATTTATCAGAGACCCTGCC  
ACCCATTCCATCTCCATCCAAGCAAACCTGAATGGCAATGAAACAACTGGAGAAGAAGGTAG  
GAGAAAGGGCGGTGAACTCTGGCTCTTTGCTGTGGACATGCGTGACCAGCAGTACTCAGGTT  
TGAGGGTTTGCAGAAAGCCAGGGAACCCACAGAGTCACCAACCCTTCATTTAACAAGTAAGA  
ATGTTAAAAAGTGAAAACAATGTAAGAGCCTAACTCCATCCCCCGTGGCCATTACTGCATAA  
AATAGAGTGCATTTGAAAT

**FIGURE 30**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624  
><subunit 1 of 1, 735 aa, 1 stop  
><MW: 80177, pI: 7.08, NX(S/T): 5  
MAARPLPVSPARALLLALAGALLAPCEARGVSLWNQGRADEVVSASVRSGDLWIPVKSFDSK  
NHPEVLNIRLQRESKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGHCIYHGHVRG  
YSDSAVSLSTCSGLRGLIVFENESYVLEPMKSATNRYKLFPAKKLKSVRGSCGSHHNTPNLA  
AKNVFPPPSQTWARRHKRETLKATKYVELVIVADNREFQRQGDLEKVKQRLIEIANHVDFK  
YRPLNIRIVLVGVEVWVNDMDKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNAQLVSGVYFQG  
TTIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFGMNHDTLDRGCSCQMAVEK  
GGCIMNASTGYFFPMVFSSCSRKDLETSLEKGMGVCLFNLPEVRESFGGQKCGNRFVEEGEE  
CDCGEPEECMNRCCNATTCTLKPDVCAHGLCCEDCQLKPAGTACRDSSNSCDLPEFCTGAS  
PHCPANVYLHDGHSCQDVDGYCYNGICQTHEQQCVTLWGPGAKPAPGICFERVNSAGDPYGN  
CGKVS KSSFAKCEMRDAKCGKIQCQGGASRPVIGTNAVSIETNIPLQQGGRILCRGTHVYLG  
DDMPDPGLVLAGTKCADGKICLNRCQNI SVFGVHECAMQCHGRGVCNNRKNCHCEAHWAPP  
FCDKFGFGGSTDSGPIRQAEARQEAAESNRERGGQEPVGSQEHASTASLTLI

**FIGURE 31**

TCCCAAGGCTTCTTGGATGGCAGATGATTNTGGGGTTTTGCATTGTTTCCCTGACAACGAAA  
ACAAAACAGTTTTTGGGGGTTTCAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGCAGAAACA  
GTGCAAGGAAGGGCAGGANTTCCTGGTTGAGNTTTTTGNTAAACATGGACATGNTTCAGTG  
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAAGGAGGA  
AGAGGACTCAAAAGTTTGGCCTTTCAGTACGCTCCACAGCAGTGGGGGAGAAGCAAGGGTT  
GGGCCAGTGTCCCCCTTCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATAACTGGTNTNT  
GGCTGCAANTTAATGCTNTGATATGGCTTTTAGCATTTATTATATGAAAATAGCAGGGTTTT  
AGTTTTTAATTTATCAGAGACCCTGCCACCCATTCCATNTCCATCCAAG

**FIGURE 32**

CATCCTGCAACATGGTGAAACACGCTGGCTAATTTTGTGTATTTTGGTAGAGATGGGA  
TTTCACCGTGTTAGCCAGGATTGTCTCAATCTGACCTCATGATCTGCCCCGCTCGGCCTCCC  
AAAGTGCTGGGATTACAGGCGAGTGCAACCACACCCGGCCACAACTTTTAAAGAAGTTAAT  
GAAACCATACTTTTACATTTTAAATGACAGGAAAATGCTCACAATAATTGTTAACCCAAAA  
TTCTGGATACAAAAGTACAATCTTTACTGTGTAAATACATGTATATGTACTATATGAAAATA  
TACCAAATATCAATAATACTTATCTCTGGGTAAAAACCTCTTCTCATACCCTGTGCTAACAA  
CTTTTAACAAAAAATTTGCATCACTTTTAAAGAATCAAGAAAAATTTCTGAAGGTCATATGGG  
ACAGAAAAAAAACCAAGGGAAAAATCACGCCACTTGGGAAAAAAGATTGGAATCTGCCT  
TTTTATAGATTTGTAATTAATAAGGTCCAGGCTTTCTAAGCAACTTAAATGTTTTGTTTCGA  
AACAAAGTACTTGTCTGGATGTAGGAGGAAAGGGAGTGATGTCACTGCCATTATGATGCCCC  
TTGAATATAAGACCCCTACTTGCTATCTCCCCTGCACCAGCCAGGAGCCACCCATCCTCCAGC  
ACACTGAGCAGCAAGCTGGACACACGGCACACTGATCCAAATGGGTAAGGGGATGGTGGCGA  
TGCTCATTCTGGGTCTGCTACTTCTGGCGCTGCTCCTACCCGTGCAGGTTTCTTCATTGT  
CCTTTAACCAGTATGCCGGAAGCTACTGCAGCCGAAACCACAAAGCCCTCCAACAGTGCCCT  
ACAGCCTACAGCCGGTCTCCTTGTGGTCTTGCTTGCCCTTCTACATCTCTACCATTAAGAGG  
CAGGTCAAGAAACAGCTACAGTTCTCCAACCCATACTAAACCCGAATCCAAATGGTGCCT  
AGAAGTTCAATGTGGCAAGGAAAAAAACCAGGTCTTCATCAAATCTACTAATTTCACTCCTT  
ATTAACAGAGAAACGCTTGAGAGTCTCAAACCTGGACTGGTTTAAAGAGCATCTGAAGGATTT  
GACTAGATGATAAATGCCTGTACTCCCAGTACTTTGGGAGGCCTAGGCCGGCGGATCACCTG  
AGGTCAGGAGTTTGAGACTAACCTGGCCAAAATGGTGAAACCCCATCTGTACTAAAAATACA  
AATATTGACTGGGCGTGGTGGTGAGTGCCTGTGATCCCAGCTACTCAGGTGGCTGAAGCAGG  
ACAATCACTTGAACTCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCGCGCTACTGCACTCTA  
GCCTAGCCTGGGCAACAGAGTGAGACTTCGTCTCAAAAAAAAAAAGCCAAGTGCAAGTGGCT  
CACGCCTGTAATCCCGGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAGGTCAGGAGATCA  
AGACCATCCTGGCTAATACAGTGAAACCCTGTCTCTACTAAAAATACAAAAAATTAGCCGGG  
GATGGTGGCAGGCACCTGGAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATAGCGTGAA  
CTCAGGAGGCGGAGCTTGCAAGTGAGCCGAGATTGCGCTACTGCACTCCAGCCTGGGCGACAG  
CGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 33**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309

><subunit 1 of 1, 67 aa, 1 stop

><MW: 6981, pI: 7.47, NX(S/T): 0

MGKGMVAMLILGLLLLALLLPVQVSSFVPLTSMPEATAAETTKPSNSALOPTAGLLVLLAL  
LHLYH



**FIGURE 34**

GCCGCGGCGAGAGCGCGCCAGCCCCGCCGCGATGCCGCGCGCCAGGACGCCTCCTCCCC  
CTGCTGGCCCCGGCCGGCGGCCCTGACTGCGCTGCTGCTGCTGCTGGGCCATGGCGGGCGG  
CGGGCGCTGGGGCGCCCGGGCCAGGAGGCGGGCGGGCGGGCGGACGGGGCCCCCGCGG  
CAGACGGCGAGGACGGACAGGACCCGCACAGCAAGCACCTGTACACGGCCGACATGTTACG  
CACGGGATCCAGAGCGCCGCGCACTTCGTTCATGTTCTTCGCGCCCTGGTGTGGACACTGCCA  
GCGGCTGCAGCCGACTTGGAATGACCTGGGAGACAAATAACAGCATGGAAGATGCCAAAG  
TCTATGTGGCTAAAGTGGACTGCACGGCCCACTCCGACGTGTGCTCCGCCAGGGGGTGGCA  
GGATACCCACCTTAAAGCTTTTCAAGCCAGGCCAAGAAGCTGTGAAGTACCAGGGTCTCG  
GGACTTCCAGACACTGGAAAAGTGGATGCTGCAGACACTGAACGAGGAGCCAGTGACACCAG  
AGCCGGAAGTGAACCGCCAGTGCCCCGAGCTCAAGCAAGGGCTGTATGAGCTCTCAGCA  
AGCAACTTTGAGCTGCACGTTGCACAAGGCGACCACTTTATCAAGTTCTTCGCTCCGTGGTG  
TGGTCACTGCAAAGCCCTGGCTCCAACCTGGGAGCAGCTGGCTCTGGGCCTTGAACATTCCG  
AAACTGTCAAGATTGGCAAGGTTGATTGTACACAGCACTATGAACCTCTGCTCCGGAAACCAG  
GTTCTGTGGCTATCCCACTCTTCTCTGGTTCCGAGATGGGAAAAAGGTGGATCAGTACAAGGG  
AAAGCGGGATTTGGAGTCACTGAGGGAGTACGTGGAGTCCGAGCTGCAGCGCACAGAGACTG  
GAGCGACGGAGACCGTCAAGCCCTCAGAGGCCCGGTGCTGGCAGCTGAGCCCGAGGCTGAC  
AAGGGCACTGTGTTGGCACTCACTGAAAATAACTTCGATGACACCATTGCAGAAGGAATAAC  
CTTCATCAAGTTTTATGCTCCATGGTGTGGTCATTGTAAGACTCTGGCTCCTACTTGGGAGG  
AACTCTCTAAAAAGGAATTCCCTGGTCTGGCGGGGGTCAAGATCGCCGAAGTAGACTGCACT  
GCTGAACGGAATATCTGCAGCAAGTATTCGGTACGAGGCTACCCACGTTATTGCTTTTCCG  
AGGAGGGAAGAAAGTCAGTGAGCACAGTGGAGGCAGAGACCTTGACTCGTTACACCGCTTTG  
TCCTGAGCCAAGCGAAAGACGAACCTTAGGAACACAGTTGGAGGTCACCTCTCCTGCCCAGC  
TCCCGCACCCCTGCGTTTAGGAGTTCAGTCCACAGAGGCCACTGGGTTCCCAAGTGGTGGCTG  
TTCAGAAAGCAGAACATACTAAGCGTGAGGTATCTTCTTTGTGTGTGTGTTTTCCAAGCCAA  
CACACTCTACAGATTCTTTATTAAGTTAAGTTTCTCTAAGTAAATGTGTAACATCATGGTCAC  
TGTGTAAACATTTTTCAGTGGCGATATATCCCCTTTGACCTTCTCTTGATGAAATTTACATGG  
TTTCCTTTGAGACTAAAATAGCGTTGAGGGAAATGAAATTGCTGGACTATTTGTGGCTCCTG  
AGTTGAGTGATTTTGGTGAAAGAAAGCACATCCAAAGCATAGTTTACCTGCCACAGAGTTCT  
GGAAAGGTGGCCTTGTGGCAGTATTGACGTTCTCTGATCTTAAGGTCACAGTTGACTCAAT  
ACTGTGTTGGTCCGTAGCATGGAGCAGATTGAAATGCAAAAACCCACACCTCTGGAAGATAC  
CTTCACGGCCGCTGCTGGAGCTTCTGTTGCTGTGAATACTTCTCTCAGTGTGAGAGGTTAGC  
CGTGATGAAAGCAGCGTTACTTCTGACCGTGCTGAGTAAGAGAATGCTGATGCCATAACTT  
TATGTGTGATACTTGTCAAATCAGTTACTGTTTACGGGGATCCTTCTGTTTCTCACGGGGTG  
AAACATGTCTTTAGTTCTTCATGTTAACACGAAGCCAGAGCCCACATGAACTGTTGGATGTC  
TTCCTTAGAAAGGGTAGGCATGGAAAATTCCACGAGGCTCATTTCTCAGTATCTCATTAACCTC  
ATTGAAAGATTCCAGTTGTATTTGTACCTGGGGTGACAAGACCAGACAGGCTTTCCAGGC  
CTGGGTATCCAGGGAGGCTCTGCAGCCCTGCTGAAGGGCCCTAACTAGAGTTCTAGAGTTTC  
TGATTCTGTTTCTCAGTAGTCCTTTTAGAGGCTTGCTATACTTGGTCTGCTTCAAGGAGGTC  
GACCTTCTAATGTATGAAGAATGGGATGCATTTGATCTCAAGACCAAAGACAGATGTCAGTG  
GGCTGCTCTGGCCCTGGTGTGCACGGCTGTGGCAGCTGTTGATGCCAGTGTCTCTAACTCA  
TGCTGTCTTGTGATTAAACACCTCTATCTCCCTTGGGAATAAGCACATACAGGCTTAAGCT  
CTAAGATAGATAGGTGTTTGTCTTTTACCATCGAGCTACTTCCCATAATAACCACTTTGCA  
TCCAACACTCTTCACCCACCTCCCATACGCAAGGGGATGTGGATACTTGGCCCAAAGTAACT  
GGTGGTAGGAATCTTAGAAACAAGACCACTTATACTGTCTGTCTGAGGCAGAAGATAACAGC  
AGCATCTCGACCAGCCTCTGCCTTAAAGGAAATCTTTATTAATCACGTATGGTTTACAGATA  
ATTCTTTTTTTTAAAAAAACCCAACCTCCTAGAGAAGCACAACCTGTCAAGAGTCTTGTACACA  
CAACTTCAGCTTTGCATCACGAGTCTTGTATTCCAAGAAAATCAAAGTGGTACAATTTGTTT  
GTTTACACTATGATACTTTCTAAATAAACTCTTTTTTTTTTAA

**FIGURE 35**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47629, pI: 5.90, NX(S/T): 0
MPARPGRLLPLLARPAALTALLLLLLLGHGGGGRWGARAQEAAAAAADGPPAADGEDGQDPHS
KHLYTADMFTHG IQSAAHFVMFFAPWCGHCQRLQPTWNDLGDKYNSMEDAKVYVAKVDCTAH
SDVCSAQGVRGYPTLKLFKPGQEAVKYQGPRDFQTLNWMQLQTLNEEPVTPEPEVEPPSAPE
LKQGLYELSASNFE LHVAQGDHF IKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCT
QHYELCSGNQVRGYPTLLWFRDGKKVDQYKGKRDLESLREYVESQLQRTETGATETVTPSEA
PVLAAEPEADKGTVLALTENNFDDTIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLA
GVKIAEVDCTAERNICSKYSVRGYPTLLLFRGGKKVSEHSGGRDLDSLHRFVLSQAKDEL
```



**FIGURE 36**

CTTTTCTGAGGAACCAACAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT  
CCTCCTGGTACTATTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTA  
CCGCTGAAGTCTGTGCCACACACACAATTTACCAGGACCCAAAGGAGATGATGGTGAAAAA  
GGAGATCCAGGAGAAGAGGGGAAAGCATGGCAAAGTGGGACGCATGGGGCCGAAAGGAATTAA  
AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTGGGAAGA  
AGGGTGACAAAGGGGAAAAAGGTTTGCTTGGAATACCTGGAGAAAAAGGCAAAGCAGGTACT  
GTCTGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCTCGGCT  
CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAACTGAAGAGAAAT  
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGG  
GGTGGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGC  
CAAGAGTGGCTTCTTTCGGGTGTTTATTGGCGTGAATGACCTTGAAAGGGAGGGACAGTACA  
TGTCCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGAC  
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG  
CCATCTTACCATGTACTTTGTCTGTGAGTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCT  
ACGTATTTGCTATTTTCCTGTGACCGTCATTACAGTTATTGTTATCCATCCTTTTTTTCCTG  
ATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT  
CCATCATCAAAAAAAAAAAAAAAAAA

**FIGURE 37**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980  
><subunit 1 of 1, 277 aa, 1 stop  
><MW: 30645, pI: 7.47, NX(S/T): 2  
MNGFASLLRRNQFILLVLFLLQIQSLGLDIDSRTAEVCATHTISPGPKGDDGEKGDGPGEEG  
KHGKVGRMGPKGIKGELGDMGDQGNIGKTGPIGKKGDKGEKGLLGIPGEKGKAGTVCDGCRY  
RKFGVQLDISIARLXTSMKFVKNVIAGIRETEEFYIIVQEEKNYRESLTHCRIRGGMLAMP  
KDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMSTDNTPLQYNSWNEGEPSDPYGHEDC  
VEMLSSGRWNDTECHLTMYFVCEFIKKKK

**FIGURE 38**

GGTTCTATCGATTCTGAATTCTGGCCACACTGGCCGGATCCTCTAGAGATCCCTCGACCTCGAC  
CCACGCGTCCGCTGCTCTCCGCCCCGTGTGGAGTGGTGGGGGCTGGGTGGGAATGGGCGTGT  
GCCAGCGCACGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTT  
CGGAAGGGAGGATCAGGGATGTTTGGGAGCGGCTGGAACCAGACGGTGCCGATAGAGGAAGC  
GGGCTCCATGGCTGCCCTCCTGCTGCTGCCCCCTGCTGCTGTTGCTACCGCTGCTGCTGCTGA  
AGCTACACCTCTGGCCGCGAGTTGCGCTGGCTTCCGGCGGACTTGGCCTTTGCGGTGCGAGCT  
CTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGCGGCTGCCGCCGACCCGGAAGC  
TCCCGAGGGGGGCTGCAGCCTGGCCTGGCGCCTCGCGGAACCTGGCCCAGCAGCGCGCCGCGC  
ACACCTTTCTCATTACGGCTCGCGGCGCTTTAGCTACTCAGAGGCGGAGCGCGAGAGTAAC  
AGGGCTGCACGCGCCTTCCTACGTGCGCTAGGCTGGGACTGGGGACCCGACGGCGGCGACAG  
CGGCGAGGGGAGCGCTGGAGAAGGCGAGCGGGCAGCGCCGGGAGCCGGAGATGCAGCGGCCG  
GAAGCGGCGCGGAGTTTGCCGGAGGGGACGGTGCCGCCAGAGGTGGAGGAGCCGCCGCCCT  
CTGTACCTGGAGCAACTGTGGCGCTGCTCCTCCCCGCTGGCCCAGAGTTTCTGTGGCTCTG  
GTTCCGGGCTGGCCAAGGCCGCGCTGCGCACTGCCTTTGTGCCACCGCCCTGCGCCGGGGCC  
CCCTGCTGCACTGCCTCCGCGAGCTGCGGCGCGCGCGCGCTGGTGCTGGCGCCAGAGTTTCTG  
GAGTCCCTGGAGCCGGACCTGCCCGCCCTGAGAGCCATGGGGCTCCACCTGTGGGCTGCAGG  
CCCAGGAACCCACCCTGCTGGAATTAGCGATTTGCTGGCTGAAGTGTCCGCTGAAGTGGATG  
GGCCAGTGCCAGGATACCTCTCTCCCCCAGAGCATAACAGACACGTGCCTGTACATCTTC  
ACCTCTGGCACCCAGGGCCTCCCCAAGGCTGCTCGGATCAGTCATCTGAAGATCCTGCAATG  
CCAGGGCTTCTATCAGCTGTGTGGTGTCCACCAGGAAGATGTGATCTACCTCGCCCTCCCAC  
TCTACCACATGTCCGGTTCCCTGCTGGGCATCGTGGGCTGCATGGGCATTGGGGCCACAGTG  
GTGCTGAAATCCAAGTTCTCGGCTGGTCACTTCTGGGAAGATTGCCAGCAGCACAGGGTGAC  
GGTGTTCAGTACATTGGGGAGCTGTGCCGATACCTTGTCAACCAGCCCCCGAGCAAGGCAG  
AACGTGGCCATAAGGTCCGGCTGGCAGTGGGCAGCGGGCTGCGCCCAGATACCTGGGAGCGT  
TTTGTGCGGCGCTTCGGGCCCCCTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACGT  
GGCCACCATCAACTACACAGGACAGCGGGGCGCTGTGGGGCGTGCTTCCTGGCTTTACAAGC  
ATATCTTCCCCTTCTCCTTGATTGCTATGATGTCAACCACAGGAGAGCCAATTCGGGACCCC  
CAGGGGCACTGTATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGGTAAGCCA  
GCAGTCCCCATTCTGGGCTATGCTGGCGGGCCAGAGCTGGCCCAGGGGAAGTTGCTAAAGG  
ATGTCTTCCGGCCTGGGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAA  
GGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTGGC  
CACAACCGAGGTGGCAGAGGTCTTCGAGGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATG  
GAGTCACTGTGCCAGGGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCC  
CACGCTTTGGACCTTATGCAGCTCTACACCCACGTGTCTGAGAACTTGCCACCTTATGCCCCG  
GCCCCGATTCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAAACAGCAGAAAG  
TTCGGATGGCAAATGAGGGCTTCGACCCACAGCACCTGTCTGACCCACTGTACGTTCTGGAC  
CAGGCTGTAGGTGCCTACCTGCCCCCTCACAACCTGCCCGGTACAGCGCCCTCCTGGCAGGAAA  
CCTTCGAATCTGAGAACTTCCACACCTGAGGCACCTGAGAGAGGAACTCTGTGGGGTGGGGG  
CCGTTGCAGGTGTACTGGGCTGTCAGGGATCTTTTCTATACCAGAACTGCGGTCACTATTTT  
GTAATAAATGTGGCTGGAGCTGATCCAGCTGTCTCTGACCTAAAAAAGGTAATAAGC  
AAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGTAGGGATAACAGGGTAATAAGC  
TTGGCCGCCATGGCCCAACTTGTTTATTGCAG

**FIGURE 39**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50913  
><subunit 1 of 1, 730 aa, 1 stop  
><MW: 78644, pI: 7.65, NX(S/T): 2  
MGVCQRTAPWKEKSQLERAAALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLLPLLLLLLPL  
LLLKLHLWPQLRWLPADLAFVRLCCKRALRARALAAAADPEGPEGGCSLAWRLAELAQQ  
RAAHTFLINGSRRFSYSEAERESNRAARAFLRALGWDWGPDGGDSGEGSAGEGERAAPGAGD  
AAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFGGLAKAGLRRTAFVPTAL  
RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA  
EVDGPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQLCGVHQEDVIYL  
ALPLYHMSGSLLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPP  
SKAERGHKVRRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRASW  
LYKHIFPFSLIRYDVTTGEPIRDPOGHCMATSPGEPGLLVAPVSQQSPFLGYAGGPFLAQQGK  
LLKDVFRPGDVFFNTGDLLVCDDQGFRLRFHDRTGDTFRWKGENVATTEVAEVFEALDFLQEV  
NVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPYARPRFLRLQESLATTETFK  
QQKVRMANEGFDPSTLSPLYVLDQAVGAYLPLTTARYSALLAGNLRI

## Signal peptide:

aa 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation site  
starting at aa 136

## CUB domain protein motif

aa 254-261

## putative AMP-binding domain signature

aa 332-343

## N-glycosylation sites

aa 37-40 and 483-486

**FIGURE 40**

CCTGTGTTAAGCTGAGGTTTTCCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACA  
CACATCCCCAAGAACCTCGAGCTCACACCAACAGACACACGCGCGCATAACACTCGCTCTC  
GCTTGTCCATCTCCCTCCCGGGGGAGCCGGCGCGCGCTCCACCTTTGCCGCACACTCCGGC  
GAGCCGAGCCCGCAGCGCTCCAGGATTCTGCGGCTCGGAACTCGGATTGCAGCTCTGAACCC  
CCATGGTGGTTTTTTTAAACACTTCTTTTCCTTCTCTTCCTCGTTTTTGATTGCACCGTTTCCA  
TCTGGGGGCTAGAGGAGCAAGGCAGCAGCCTTCCCAGCCAGCCCTTGTTGGCTTGCCATCGT  
CCATCTGGCTTATAAAAGTTTGCTGAGCGCAGTCCAGAGGGCTGCGCTGCTCGTCCCCCTCGG  
CTGGCAGAAGGGGGGTGACGCTGGGCAGCGGCGAGGAGCGCGCCGCTGCCCTCTGGCGGGCTTT  
CGGCTTGAGGGGCAAGGTGAAGAGCGCACCGGCCGTGGGGTTTACCGAGCTGGATTTGTATG  
TTGCACCATGCTTCTTGGATCGGGGCTGTGATTCTTCCCCCTCTTGGGGCTGCTGCTCTCCC  
TCCCCGCGGGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTCCGCCAGGCGTACGGTGCC  
AAGGGATTGAGCCTGGCGGACATCCCCTACCAGGAGATCGCAGGGGAACACTTAAGAATCTG  
TCCTCAGGAATATACATGCTGCACCACAGAAATGGAAGACAAGTTAAGCCAACAAAGCAAAC  
TCGAATTTGAAAACCTTGTGGAAGAGACAAGCCATTTTGTGCGCACCACTTTTGTGTCCAGG  
CATAAGAAATTTGACGAATTTTTCCGAGAGCTCCTGGAGAATGCAGAAAAGTCACTAAATGA  
TATGTTTGTACGGACCTATGGCATGCTGTACATGCAGAATTCAGAAGTCTTCCAGGACCTCT  
TCACAGAGCTGAAAAGGTACTACACTGGGGGTAATGTGAATCTGGAGGAAATGCTCAATGAC  
TTTTGGGCTCGGCTCCTGGAACGGATGTTTCAGCTGATAAACCCCTCAGTATCACTTCAGTGA  
AGACTACCTGGAATGTGTGAGCAAATACACTGACCAGCTCAAGCCATTTGGAGACGTGCCCC  
GGAAACTGAAGATTGAGGTTACCCGCGCCTTCATTGCTGCCAGGACCTTTGTCCAGGGGCTG  
ACTGTGGGCAGAGAAGTTGCAAACCGAGTTTCCAAGGTCAGCCCAACCCCAAGGTTGTATCCG  
TGCCCTCATGAAGATGCTGTACTGCCCATACTGTGCGGGGCTTCCCACTGTGAGGCCCTGCA  
ACAATACTGTCTCAACGTATGAAGGGCTGCTTGGCAAATCAGGCTGACCTCGACACAGAG  
TGAATCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGACTGGAGGGGCCATTCAACAT  
TGAGTCGGTCATGGACCCGATAGATGTCAAGATTTCTGAAGCCATTATGAACATGCAAGAAA  
ACAGCATGCAGGTGTCTGCAAAGGTCTTTCAGGGATGTGGTCAGCCCAAACCTGCTCCAGCC  
CTCAGATCTGCCCCGCTCAGCTCCTGAAAATTTTAATACACGTTTTCAGGCCCTACAATCCTGA  
GGAAAGACCAACAACCTGCTGCAGGCACAAGCTTGGACCGGCTGGTCACAGACATAAAAGAGA  
AATTGAAGCTCTCTAAAAGGTCTGGTCAGCATTACCTACACTATCTGCAAGGACGAGAGC  
GTGACAGCGGGCACGTCCAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACTT  
GCCTGAGATCATGAATGATGGGCTCACCAACCAGATCAACAATCCCGAGGTGGATGTGGACA  
TCACTCGGCCTGACACTTTCATCAGACAGCAGATTATGGCTCTCCGTGTGATGACCAACAAA  
CTAAAAAACGCCTACAATGGCAATGATGTCAATTTCCAGGACACAAGTGATGAATCCAGTGG  
CTCAGGGAGTGGCAGTGGGTGCATGGATGACGTGTGTCCACGGAGTTTGAGTTTGTACCA  
CAGAGGCCCCCGCAGTGGATCCCGACCGGAGAGAGGTGGACTCTTCTGCAGCCAGCGTGGC  
CACTCCCTGCTCTCCTGGTCTCTCACCTGCATTGTCTGGCACTGCAGAGACTGTGCAGATA  
ATCTTGGGTTTTTTGGTCAGATGAACTGCATTTTAGCTATCTGAATGGCCAACTCACTTCTT  
TTCTTACACTCTTGGACAATGGACCATGCCACAAAACCTTACCGTTTTCTATGAGAAGAGAG  
CAGTAATGCAATCTGCCTCCCTTTTTGTGTTTTCCCAAAGAGTACCGGGTGCCAGACTGAACTG  
CTTCCTCTTTCCTTCAGCTATCTGTGGGGACCTTGTTTATTCTAGAGAGAATTCTTACTCAA  
ATTTTTCGTACCAGGAGATTTTCTTACCTTCATTTGCTTTTATGCTGCAGAAGTAAAGGAAT  
CTCACGTTGTGAGGGTTTTTTTTTTCTCATTTAAAT



**FIGURE 41**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914

><subunit 1 of 1, 555 aa, 1 stop

><MW: 62736, pI: 5.36, NX(S/T): 0

MPSWIGAVILPLLGLLLSLPAGADVKA RSCGEVRQAYGAKGFS LADIPYQEIAGEHLRICPQ  
EYTCCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENAEKSLNDMF  
VRTYGMLYMQNSEVFQDLFTTELKRYYTGGNVNLEEMLNDFWARLLERMFQLINPOYHFSEY  
LECVSKYTDQLKPFQGDVPRKLKIQVTRAFIAARTFVQGLTVGREVANRVSKVSPTPGCIRAL  
MKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNLFIDAMLLVAERLEGPFNIES  
VMDPIDVKISEAIMNMQENSMQVSAKVFGCGQPKPAPALRSARSAPENFNTRFRPYNPEER  
PTTAAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDESVTAGTSNEEECWNGHASKARYLPE  
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG  
SGSGCMDDVCPTEFEFVTTEAPAVDPDRREVDSSAAQRGHSLLSWSLTCIVLALQRLCR

## FIGURE 42A

CGGACGCGTGGGCGGACGCGTGGGCAAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCT  
GAGAAAACGCACGCAGTTTGCAGCGCCTGCGCCGGGTGCGCCAACCTACGCAAAGACCAAGCG  
GGCTCCGCGCGGACCCGCGCGGGCTAGGGACCCGGCTTTGGCCTTCAGGCTCCCTAGCAG  
CGGGGAAAAGGAATTGCTGCCCGGAGTTTCTGCGGAGGTGGAGGGAGATCAGGAAACGGCTT  
CTTCCTCACTTCGCGCGCCTGGTGAGTGTGCGGGGAGATTGGCAAACGCCTAGGAAAGGACTGG  
GGAAAATAGCCCTGGGAAAGTGGAGAAGGTGATCAGGAGGCCGGTCCACTACGGCAGTTTAT  
CTGTCTGATCAGAGCCAGACGCGACGCGTCCACTTCGCAGTTCTTTCCAGGTGTGGGGACCG  
CAGGACAGACGGCCGATCCCGCCGCCCTCCGTACCAGCACTCCAGGAGAGTCAGCCTCGCT  
CCCCAACGTCGAGGGCGCTCTGGCCACGAAAAGTTCTGTCCACTGTGATTCTCAATTCCTT  
GCTTGGTTTTTTTTCTCCAGAGAACTTTTGGGTGGAGATATTAACCTTTTTCTTTTTTTTTT  
CCTTGGTGGAAGCTGCTCTAGGGAGGGGGGAGGAGGAGGAGAAAGTGAAATGTGCTGGAGAA  
GAGCGAGCCCTCCTTGTTCCTCCGGAGTCCCATCCATTAAGCCATCACTTCTGGAAGATTAA  
AGTTGTGCGGACATGGTGACAGCTGAGAGGAGAGGAGGATTCTTGCCAGGTGGAGAGTCTTC  
ACCGTCTGTTGGGTGCATGTGTGCGCCCGCAGCGGCGCGGGGCGCGTGGTTCTCCGCGTGGA  
GTCTCACCTGGGACCTGAGTGAATGGCTCCAGGGGCTGTGCGGGGCATCCGCCTCCGCCTT  
CTCCACAGGCCTGTGTCTGTCTGGAAAGATGCTAGCAATGGGGGCGCTGGCAGGATTCTGG  
ATCCTCTGCCTCCTCACTTATGGTTACCTGTCTGGGGCCAGGCCTTAGAAGAGGAGGAAGA  
AGGGGCCTTACTAGCTCAAGCTGGAGAGAACTAGAGCCCAGCACAACTTCCACCTCCCAGC  
CCCATCTCATTTTTCATCCTAGCGGATGATCAGGGATTTAGAGATGTGGGTACCACGGATCT  
GAGATTAAAACACCTACTCTTGACAAGCTCGCTGCCGAAGGAGTTAACTGGAGAACTACTA  
TGTCCAGCCTATTTGCACACCATCCAGGAGTCAGTTTATTACTGGAAAGTATCAGATACACA  
CCGGACTTCAACATTCTATCATAAGACCTACCCAACCCAACCTGTTTACCTCTGGACAATGCC  
ACCCTACCTCAGAACTGAAGGAGGTTGGATATTCAACGCATATGGTTCGGAATGGCACTT  
GGGTTTTAACAGAAAAGAATGCATGCCACCAGAAGAGGATTTGATACCTTTTTTGGTTCCC  
TTTTGGGAAGTGGGGATTACTATACACACTACAAATGTGACAGTCCTGGGATGTGTGGCTAT  
GACTTGTATGAAAACGACAATGCTGCCTGGGACTATGACAATGGCATATACTCCACACAGAT  
GTACACTCAGAGAGTACAGCAAATCTTAGCTTCCCATAACCCCAAAAGCCTATATTTTTAT  
ATACTGCCTATCAAGCTGTTTCACTCACCAGCTGCAAGCTCCTGGCAGGTATTTGCAACACTAC  
CGATCCATTATCAACATAAACAGGAGAAGATATGCTGCCATGCTTTCTGCTTAGATGAAGC  
AATCAACAACGTGACATTGGCTCTAAAGACTTATGGTTTTCTATAACAACAGCATTATCATTT  
ACTCTTCAGATAATGGTGGCCAGCCTACGGCAGGAGGGAGTAACTGGCCTCTCAGAGGTAGC  
AAAGGAACATATTGGGAAGGAGGGATCCGGGCTGTAGGCTTTGTGCATAGCCCACTTCTGAA  
AAACAAGGGAACAGTGTGTAAGGAACCTTGTGCACATCACTGACTGGTACCCCACTCTCATTT  
CACTGGCTGAAGGACAGATTGATGAGGACATTCAACTAGATGGCTATGATATCTGGGAGACC  
ATAAGTGAGGGTCTTCGCTCACCCCGAGTAGATATTTTGCATAACATTGACCCCTATACACC  
AAGGCAAAAAATGGCTCCTGGGCAGCAGGCTATGGGATCTGGAACACTGCAATCCAGTCAGC  
CATCAGAGTGCAGCACTGGAAATTGCTTACAGGAAATCCTGGCTACAGCGACTGGGTCCCCC  
CTCAGTCTTTCAGCAACCTGGGACCGAACC GGTTGGCACAATGAACGGATCACCTTGTCAACT  
GGCAAAAGTGTATGGCTTTTCAACATCACAGCCGACCCATATGAGAGGGTGGACCTATCTAA  
CAGGTATCCAGGAATCGTGAAGAAGCTCCTACGGAGGCTCTCACAGTTCAACAAAACCTGCAG  
TGCCGGTCAAGGTATCCCCCAAGACCCCAAGTAACCCTAGGCTCAATGGAGGGGTCTGG  
GGACCATGGTATAAAGAGGAAACCAAGAAAAAGCAAGCAAAAATCAGGCTGAGAAAAA  
GCAAAAGAAAAGCAAAAAAAGAAGAAGAAACAGCAGAAAGCAGTCTCAGGTAAACCAGCAA  
ATTTGGCTCGATAATATCGCTGGCCTAAGCGTCAGGCTTGTTTTTCATGCTGTGCCACTCCAG  
AGACTTCTGCCACCTGGCCGCCCACTGAAAACCTGTCTGCTCAGTGCCAAGGTGCTACTCT  
TGCAAGCCACACTTAGAGAGAGTGGAGATGTTTTATTTCTCTCGCTCCTTTAGAAAACGTGGT  
GAGTCTGAGTTCCACTGCTGTGCTTCAGTCAACTGACCAAACTGCTTTGAATTATAGGA  
GGAGAACAATAACCTACCATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGGTAGCATGA  
TTAAAACCTACCTTTGATAAATTACAGTCAAAGATTGTGTCACCTCAAAGGCCTTGAAGAATA  
TATTTTCTTGGTGAATTTTTGTATGTCTGTCAATGACACTTGGGTTTTTTAATTAATTCTA  
TTTTATATATATAAATATATGTTTCTTTTCTGTGAAAAGCTGTTTTTCTCACATGTGAACA  
GCTTGCACCTCATTTTACCATGCGTGAGGGAATGGCAAATAAGAATGTTTGAGCACACTGCC  
CACAATGAATGTAACCTATTTTCTAAACACTTTACTAGAAGAACATTTTCAGTATAAAAAACCT  
AATTTATTTTTACAGAAAAATATTTTGTGTTTTTATAAAAAGTTATGCAAATGACTTTTAT  
TTTTATTTCTGCTACATACCATAGAAGAATTTTATTTTCAATTTCTTCAAATTATCAAGCACTGT  
AATACTATAAATTAATGTAATACTGTGTGAATTCAGACTATAAAAAACATCATTACAGAAAC  
TTTATAATCGTCATTGTTCAATCAAGATTTTGAATGTAATAAGATGAATATATTCCTTACAA

**FIGURE 42B**

ATTACTTGGAAATTCAATGTTTGTGTCAGAGTTGAGACAACTTTATTGTTTCTATCATAAACT  
ATTTATGTATCTTAATTATTAATAATGATTTACTTTATGGCACTAGAAAATTTACTGTGGCTT  
TTCTGATCTAACTTCTAGCTAAAATTGTATCATTGGTCCTAAAAATAAAAATCTTTACTAA  
TAGGCAATTGAAGGAATGGTTTGCTAACAACACAGTAATATAATATGATTTTACAGATAGA  
TGCTTCCCCTTGGCTATGACATGGAGAAAGATTTTCCCATAATAATACTAATATTTATATT  
AGGTTGGTGCAAACTAGTTGCGGTTTTTCCCATTAAGTAATAACCTTACTCTTATACAA  
AGTGGACACTGTGGGGAGATACAGAGAAATGGAAGATACGGATCCTGCCTGGAGTAGGTAAC  
CTTGCTTGGAAACCCACATGCAAACGTCATGAGGAGAATTAAAGGAGTATTATCAGTAATG  
AAGTTTATCATGGGTCAATGAGCATAGATTGGTGTGGATCCTGTAGACCCTGGTGTTTT  
CTTTGAAGTGCCCTCTCCTAATGCAGAGGCCTTGAAGCTTACAGTATACACTTGAAAAGTCA  
CAGATAGCTAGAATTATGATCTTTGAAGTTATAACTGTGATCTGAAAATGTGTGTGGTGGTA  
TGACAGCATACCATTAATAACATTTACATCACAGCTCAAAGGACTGTGATATAATCCATTTA  
TATCACAACCTCAAAGGACTGTGATATAATCCATTTATATCACAGCTCACAGTTTCTGAAAAT  
GTATAAAAGAATCTATAATCTAGTACTGAAATTACTAAATTGGGTAAGATGATTTAAATGAT  
TTTAATTTTAACATTTTATTTCTAGAATATATGGCTCCATTTTATTTTATAGTGTAAGTTG  
TATTTCTAAAGTTTGTGTTTTGTGCGACAGTATCTTTTAAATGAGTCTTAAAAATAAAGGCA  
TATTGTTTCATGTTTAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAA



**FIGURE 43**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296

><subunit 1 of 1, 515 aa, 1 stop

><MW: 56885, pI: 6.49, NX(S/T): 5

MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTGYLSWGQALEEEEEEGALLAQA  
GEKLEPSTTSTSQPHLIFILADDQGFDRDVGYPHGSEIKTPTLDKLAAGVKLENYYVQPICTP  
SRSQFITGKYQIHTGLQHSIIRPTQPNCLPLDNATLPQKLKEVGYSTHMGKWHLGFNKREC  
MPTRRGFDTFFGSLLGSGDYTHYKCDSPGMCGYDLYENDNAAWDYDNGIYSTQMYTQRVQQ  
ILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIININRRRYAAMLSCLDEAINNVTLA  
LKTYGFYNNSSIIYSSDNGGQPTAGGSNWPLRGSKGTYWEGGIRAVGVHSPLLKNKGTVCK  
ELVHITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPG  
QQAMGSGTLQSSQPSECSTGNCLQEILATATGSPLSLSATWDRTGGTMNGSPCQLAKVYGFS  
TSQPTHMRGWTYLTGIQES

**Important Features:**

**Signal Peptide:**

amino acids 1-37

**Sulfatases signature 1.**

amino acids 120-132

**Sulfatases signature 2.**

amino acids 168-177

**Tyrosine kinase phosphorylation site.**

amino acids 163-169

**N-glycosylation sites.**

amino acids 157-160, 306-309 and 318-321

**FIGURE 44**

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGGC  
TTAGCTGCTACGGGGTCCGGCCGGCGCCCTCCCGAGGGGGGCTCAGGAGGAGGAAGGAGGAC  
CCGTGCGAGAATGCCTCTGCCCTGGAGCCTTGCGCTCCCGCTGCTGCTCTCCTGGGTGGCAG  
GTGGTTTCGGGAACGCGGCCAGTGCAAGGCATCACGGGTTGTTAGCATCGGCACGTCAGCCT  
GGGTCTGTCACTATGGAACATAACTGGCCTGCTGCTACGGCTGGAGAAGAAACAGCAAGGG  
AGTCTGTGAAGCTACATGCGAACCTGGATGTAAGTTTGGTGAGTGCGTGGGACCAAACAAT  
GCAGATGCTTTCCAGGATACACCGGGAAACCTGCAGTCAAGATGTGAATGAGTGTGGAATG  
AAACCCCGGCCATGCCAACACAGATGTGTGAATACACACGGAAGCTACAAGTGCTTTTGCCT  
CAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAACCTTAGGACATGTGCCATGATAA  
ACTGTCAGTACAGCTGTGAAGACACAGAAGAAGGGCCACAGTGCCCTGTGTCCATCCTCAGGA  
CTCCGCTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT  
CATCTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTACTGCAAATGTCACA  
TTGGTTTCGAACTGCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACT  
ATGGATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAAGGGTCCTTCAAGTG  
TAAATGCAAGCAGGGATATAAAGGCAATGGACTTCGGTGTCTGCTATCCCTGAAAATTCTG  
TGAAGGAAGTCCTCAGAGCACCTGGTACCATCAAAGACAGAATCAAGAAGTTGCTTGCTCAC  
AAAAACAGCATGAAAAAGAAGGCCAAAAATTAAAAATGTTACCCAGAACCCACCAGGACTCC  
TACCCCTAAGGTGAACTTGCGAGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGCGGGAAC  
CTCATGGAGGTAAAAAAGGGAATGAAGAGAAATGAAGAGGGGCTTGAGGATGAGAAAAGAG  
AAGAGAAAGCCCTGAAGAATGACATAGAGGAGCGAAGCCTGCGAGGAGATGTGTTTTTCCCT  
AAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCTGGTCCAAAGGAAAGCGCTAACTTCCAA  
ACTGGAACATAAAGATTTAAATATCTCGGTGACTGCAGCTTCAATCATGGGATCTGTGACT  
GGAAACAGGATAGAGAAGATGATTTTGAAGTGAATCCTGCTGATCGAGATAATGCTATTGGC  
TTCTATATGGCAGTTCCGGCCTTGGCAGGTCAAGAAAGACATTGGCCGATTGAACTTCT  
CCTACCTGACCTGCAACCCCAAGCAACTTCTGTTTGCTCTTTGATTACCGGCTGGCCGGAG  
ACAAAGTCGGGAACTTCGAGTGTGTGAAAAACAGTAACAATGCCCTGGCATGGGAGAAG  
ACCACGAGTGAGGATGAAAAGTGGAAGACAGGGAAATTCAGTTGTATCAAGGAAGTATGC  
TACCAAAGCATCATTTTTGAAGCAGAACGTGGCAAGGGCAAACCGGCGAAATCGCAGTGG  
ATGGCGTCTTGCTTGTTTCAGGCTTATGTCCAGATAGCCTTTTATCTGTGGATGACTGAATG  
TTACTATCTTTATATTTGACTTTGTATGTCAGTTCCCTGGTTTTTTTGATATTGCATCATAG  
GACCTCTGGCATTTTAGAATTACTAGCTGAAAAATTGTAATGTACCAACAGAAATATTATTG  
TAAGATGCCTTTCTTGATATAAGATATGCCAATATTTGCTTTAAATATCATATCACTGTATCT  
TCTCAGTCATTTCTGAATCTTTCCNCATTATATTATAAAATNTGGAAANGTCAGTTTATCTC  
CCCTCCTCNGTATATCTGATTTGTATANGTANGTTGATGNGCTTCTCTCTACAACATTTCTA  
GAAAATAGAAAAAAAAGCACAGAGAAATGTTAACTGTTTGACTCTTATGATACTTCTTGA  
AACTATGACATCAAAGATAGACTTTTGCCTAAGTGGCTTAGCTGGGTCTTTCATAGCCAAAC  
TTGTATATTTAATTCTTTGTAATAATAA

**FIGURE 45**

MPLPWSLALPLLLSWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRNRNSKGVCE  
ATCEPGCKFGECVGPNNKCRCPGYTGKTCSQDVNECGMKPRPCQHRNVNTHGSYKCFCLSGH  
MLMPDATCVNSRTCAMINCOYSCEDTEEGPQCLCPSSGLRLAPNGRDCLDIDECASGKVICP  
YNRRVCNVTFGSYYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKCK  
QGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMKKKAKIKNVTPEPTRTPK  
VNLQPFNYEEIVSRGGNSHGKKGNEEK

Signal peptide:

amino acids 1-21

EGF-like domain cysteine pattern signature.

amino acids 80-91

Calcium-binding EGF-like domains

amino acids 103-124, 230-251 and 185-206

**FIGURE 46**

GGGAGCTGCTGCTGTGGCTGCTGGTGCTGTGCGCGCTGCTCCTGCTCTTGGTGCAGCTGCTG  
CGCTTCCTGAGGGCTGACGGCGACCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCCC  
AGAATGGGAGCTGACTGATATGGTGGTGTGGGTGACTGGAGCCTCGAGTGGAATTGGTGAGG  
AGCTGGCTTACCAGTTGTCTAAACTAGGAGTTTCTCTTGTGCTGTCAGCCAGAAGAGTGCAT  
GAGCTGGAAAGGGTGAAAAGAAGATGCCTAGAGAATGGCAATTTAAAAGAAAAAGATATACT  
TGTTTTGCCCCCTTGACCTGACCGACACTGGTTCCCATGAAGCGGCTACCAAAGCTGTTCTCC  
AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGGAATGTCCCAGCGTTCTCTGTGC  
ATGGATACCAGCTTGGATGTCTACAGAAAGCTAATAGAGCTTAACCTACTTAGGGACGGTGTC  
CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA  
ATAGCATCCTGGGTATCATATCTGTACCTCTTTCCATTGGATACTGTGCTAGCAAGCATGCT  
CTCCGGGGTTTTTTTAATGGCCTTCGAACAGAACTTGCCACATACCCAGGTATAATAGTTTC  
TAACATTTGCCCAGGACCTGTGCAATCAAATATTGTGGAGAATTCCTAGCTGGAGAAGTCA  
CAAAGACTATAGGCAATAATGGAGACCAGTCCCAAGATGACAACCAGTCGTTGTGTGCGG  
CTGATGTTAATCAGCATGGCCAATGATTTGAAAGAAGTTTGGATCTCAGAACAACCTTTCTT  
GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCCTGGTGGATAACCAACAAGATGG  
GGAAGAAAAGGATTGAGAACTTTAAGAGTGGTGTGGATGCAGACTCTTCTTATTTTAAAATC  
TTTAAGACAAAACATGACTGAAAAGAGCACCTGTACTTTTCAAGCCACTGGAGGGAGAAATG  
GAAAACATGAAAACAGCAATCTTCTTATGCTTCTGAATAATCAAAGACTAATTTGTGATTTT  
ACTTTTAAATAGATATGACTTTGCTTCCAACATGGAATGAAATAAAAAATAAATAATAAAAG  
ATTGCCATGAATCTTGCAAAA

**FIGURE 47**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA36343  
><subunit 1 of 1, 289 aa, 1 stop  
><MW: 32268, pI: 9.21, NX(S/T): 0  
MVVWVTGASSGIGEELAYQLSKLGVSLVLSARRVHELERVKRRCLENGNLKEKDILVLPLDL  
TDTGSHEAATKAVLQEFGRIDILVNNGGMSQRSCLMDTSLDVYRKLIELNYLGTVSLTKCVL  
PHMIERKQGKIVTVNSILGIIISVPLSIGYCASKHALRGFFNGLRTELATYPGIIIVSNICPGP  
VQSNIVENSLAGEVTKTIGNNGDQSHKMTTSRCVRLMLISMANDLKEVWISEQPFLLVTYLW  
QYMPWAWWITNKMGGKRIENFKSGVDADSSYFKIFKTKHD

**Important Features:****Signal Peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 136-157

**Tyrosine kinase phosphorylation site.**

106-113 and 107-114

**Homologous region to Short-chain alcohol dehydrogenase**

amino acids 80-90, 131-168, 1-13 and 176-185

**FIGURE 48**

GCGACGTGGGCACCGCCATCAGCTGTTGCGCGCTCTTCTCCTCCAGGTGGGGCAGGGGTTTC  
GGGCTGGTGGAGCATGTGCTGGGACAGGACAGCATCCTCAATCAATCCAACAGCATATTCGG  
TTGCATCTTCTACACACTACAGCTATTGTTAGGTTGCCTGCGGACACGCTGGGCCTCTGTCC  
TGATGCTGCTGAGCTCCCTGGTGTCTCTCGCTGGTTCTGTCTACCTGGCCTGGATCCTGTTT  
TTCGTGCTCTATGATTTCTGCATTGTTTGTATCACCACCTATGCTATCAACGTGAGCCTGAT  
GTGGCTCAGTTTCCGGAAGGTCCAAGAACCCAGGGCAAGGCTAAGAGGCACTGAGCCCTCA  
ACCCAAGCCAGGCTGACCTCATCTGCTTTGCTTTGGTCTTCAAGCCGCTCAGCGTGCCTGTG  
GACAGCGTGGCCCCGGCCCCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCC  
TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCACATCTGCAGCGGCTCCCTGGTGGCAGACAC  
CTGGGTCTTCACTGCTGCCCACTGCTTTGAAAAGGCAGCAGCAACAGAACTGAATTCCTGGT  
CAGTGGTCTTGGGTTCTCTGCAGCGTGAAGGACTCAGCCCTGGGGCCGAAGAGGTGGGGGTG  
GCTGCCCTGCAGTTGCCCAGGGCCTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGCT  
GCAGCTCGCCCCACCCACGACCCACACACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCC  
CCTTTGGAGCCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCAGTGATGCTCCTGGGACC  
CTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAAGTGTATCTACAACCAGCT  
GCACCAGCGACACCTGTCCAACCCGGCCCCGGCCTGGGATGCTATGTGGGGGCCCCCAGCCTG  
GGGTGCAGGGCCCCCTGTCAGGGAGATTCCGGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGA  
CACTGGGTTCAGGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGT  
GCTGCTGACCAACACAGCTGCTCACAGTTCTTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTT  
TCCTGGCCCAGAGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGA  
TCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCCCTCCCCATGGCCCTGGGAGGCCAGGCT  
GATGCACCAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGGCGGTGCTAACTG  
CTGCCCCACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGA  
CCGGAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGG  
CTACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCC  
TCTGCCTGCCCTATCCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTTCTGGGACGG  
GCCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGGCCTAG  
GGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGG  
TGTGTACCAGTGCTGTGGGTGAGCTGCCCAGCTGTGAGGGCCTGTCTGGGGCACCCTGGTG  
CATGAGGTGAGGGGCACATGGTTCTTGGCCGGGCTGCACAGCTTCGGAGATGCTTGCCAAGG  
CCCCGCCAGGCCGGCGGTCTTACC CGCTCCCTGCCTATGAGGACTGGGTGAGCAGTTTGG  
ACTGGCAGGTCTACTTCGCCGAGGAACCAGAGCCCGAGGCTGAGCCTGGAAGCTGCCTGGCC  
AACATAAGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTCTCAGGACAAGAGAATGC  
AGGCAGGCAAATGGCATTACTGCCCTGTCTCCCCACCCCTGTGATGTGTGATTCCAGGCAC  
CAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCTGCCTGGGGCCACAGGTGCCCA  
CTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCCACACCCAACTCTGCTACCAAGC  
AGGCGTCTCAGCTTTCTCTCCTCTTTACTCTTTTCAGATACAATCACGCCAGCCACGTTGTTT  
TGAAAATTTCTTTTTTTGGGGGGCAGCAGTTTTCTTTTTTTAACTTAAATAAATTGTTAC  
AAAATAAAA



**FIGURE 49**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40571  
MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQ GKAKRHGNTV  
PGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAATELNSWSVVLGSLQREGLSPGA  
EEVGVAALQLPRAYNHYSQGS DLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATGWDQDTS  
DAPGTLRLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGD SGGPVLC  
LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGA AFLAQSPETPEMSDEDS  
CVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAPEEWSV  
GLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHL PDGERG  
WVLGRARPGAGISSLQTVPVTLGPRACSR LHAAPGGDGSPILPGMVCTSAVGELPSCEGLS  
GAPLVHEVRGTWFLAGLHSFGDACQGPAPPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEP  
GSCLANISQPTSC

**Important features:****Signal peptide:**

amino acids 1-15

**Homologous region to Serine proteases, trypsin family**

amino acids 79-95, 343-359 and 237-247

**N-glycosylation sites.**

amino acids 37-40 and 564-567

**Kringle domains**

amino acids 79-96, 343-360 and 235-247

**FIGURE 50**

CGGGCCGCCCCCGGCCCCCATTGCGGGCCGGCCTCGCTGCGGCGGCGACTGAGCCAGGCTGG  
GCCGCGTCCCTGAGTCCCAGAGTCGGCGCGGGCGGGCAGGGGCAGCCTTCCACCACGGGGAG  
CCCAGCTGTCAGCCGCCTCACAGGAAGATGCTGCGTCGGCGGGGCAGCCCTGGCATGGGTGT  
GCATGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAGG  
TCCCTGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCCTGTGCTGCTCCTTCTCC  
CCTGAGCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATAACAAACA  
GCTGGTGCACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCC  
TCTTCCCGACCTGCTGGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCGTGCCTGTGGCG  
GACGAGGGCAGCTTCACCTGCTTCGTGAGCATCCGGGATTTCCGGCAGCGCTGCCGTGAGCCT  
GCAGGTGGCCGCTCCCTACTCGAAGCCCAGCATGACCCTGGAGCCCAACAAGGACCTGCGGC  
CAGGGGACACGGTGACCATCACGTGCTCCAGCTACCAGGGCTACCCTGAGGCTGAGGTGTTT  
TGGCAGGATGGGCAGGGTGTGCCCTGACTGGCAACGTGACCACGTGCGAGATGGCCAACGA  
GCAGGGCTTGTTTGATGTGCACAGCGTCCTGCGGGTGGTGTGCTGGGTGCGAATGGCACCTACA  
GCTGCCTGGTGCACAACCCCGTGCTGCAGCAGGATGCGCACRGCTCTGTCAACCATCACAGGG  
CAGCCTATGACATTCCCCCAGAGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCAT  
TGCACTGCTGGTGGCCCTGGCTTTCGTGTGCTGGAGAAAGATCAAACAGAGCTGTGAGGAGG  
AGAATGCAGGAGCTGAGGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCT  
CTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCCTGACCATGAGGACCAGG  
GAGCTGCTACCCCTCCCTACAGCTCCTACCCTCTGGCTGCAATGGGGCTGCACTGTGAGCCC  
TGCCCCCAACAGATGCATCCTGCTCTGACAGGTGGGCTCCTTCTCCAAAGGATGCGATACAC  
AGACCACTGTGCAGCCTTATTTCTCCAATGGACATGATTCCCAAGTCATCCTGCTGCCTTTT  
TTCTTATAGACACAATGAACAGACCACCCACAACCTTAGTTCTCTAAGTCATCCTGCCTGCT  
GCCTTATTTACAGTACATACATTTCTTAGGGACACAGTACACTGACCACATCACCACCCTC  
TTCTTCCAGTGCTGCGTGGACCATCTGGCTGCCTTTTTTTCTCCAAAGATGCAATATTCAGA  
CTGACTGACCCCTGCCTTATTTACCAAAGACACGATGCATAGTCACCCCGGCCTTGTTTC  
TCCAATGGCCGTGATACACTAGTGATCATGTTGAGCCCTGCTTCCACCTGCATAGAATCTTT  
TCTTCTCAGACAGGGACAGTGCGGCCTCAACATCTCCTGGAGTCTAGAAGCTGTTTCCTTTC  
CCCTCCTTCCTCCCTGCCCCAAGTGAAGACAGGGCAGGGCCAGGAATGCTTTGGGGACACCG  
AGGGGACTGCCCCCACCACCATGGTGCTATTCTGGGGCTGGGGCAGTCTTTTCTGGC  
TTGCCTCTGGCCAGCTCCTGGCCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCCTTCCG  
GATGTCATCTCTCCCTGCCCCAGGAATGGAAGATGTGAGGACTTCTAATTTAAATGTGGGAC  
TCGGAGGGATTTTGTAAGTGGGGGTATATTTTGGGGAAAATAAATGTCTTTGTAAAAAAA  
AAAAAAA



**FIGURE 51**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386

><subunit 1 of 1, 316 aa, 1 stop, 1 unknown

><MW: -1, pI: 4.62, NX(S/T): 4

MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTDATLCCSFSPPEPGFSLAQ  
LNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNASLRLQVRVADEGSFTCFV  
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQGVPL  
TGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEA  
LWVTVGLSVCLIALLLVALAFVCWRKIKQSCEEENAGAEDQDGE GEGSKTALQPLKHSDSKED  
DGQEIA

**Important features:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 251-270

**N-glycosylation site.**

amino acids 91-94, 104-107, 189-192 and 215-218

**Homologous region to Immunoglobulins and MHC**

amino acids 217-234

**FIGURE 52**

TTCGTGACCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTC  
CTGAACTTGTCTGAAGCCCTTGTCCGTAAGCCTTGAAGTACGTTCTTAAATCTATGAAGTCG  
AGGGACCTTTCGCTGCTTTTGTAGGGACTTCTTTCCTTGCTTCAGCAACATGAGGCTTTTCT  
TGTGGAACGCGGTCTTGACTCTGTTTCGTCACTTCTTTGATTGGGGCTTTGATCCCTGAACCA  
GAAGTGAAAATTGAAGTTCTCCAGAAGCCATTTCATCTGCCATCGCAAGACCAAAGGAGGGGA  
TTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTC  
ACAAACATAACAATGGTCAGCCCATTTGGTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGT  
TGGGACCAGGGCTTGAAAGGAATGTGTGTAGGAGAGAAGAGAAAGCTCATCATTCCTCCTGC  
TCTGGGCTATGGAAAAGAAGGAAAAGGTAAATTTCCCCCAGAAAGTACACTGATATTTAATA  
TTGATCTCCTGGAGATTCGAAATGGACCAAGATCCCATGAATCATTCCAAGAAATGGATCTT  
AATGATGACTGGAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGTTTGAAAA  
ACATGGTGCGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTTGATAAAG  
AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTA  
TAGAGATACATCTACCCTTTTAAATATAGCACTCATCTTTCAAGAGAGGGCAGTCATCTTTAA  
AGAACATTTTATTTTTATACAATGTTCTTTCTTGCTTTGTTTTTTATTTTTATATATTTTTT  
CTGACTCCTATTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTTCTTTCTGATAAGTTATT  
GGGAAGAAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTCACTTTCACAG  
ATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAATGTTGCAACTGGGAATATACC  
ACGACATGAGACCAGGTTATAGCACAAATTAGCACCCCTATATTTCTGCTTCCCTCTATTTTC  
TCCAAGTTAGAGGTCAACATTTGAAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTCAT  
GTTATAATGAAATAGTTTATGTGTAAGTGGCTCTGAGTCTCTGCTTGAGGACCAGAGGAAAA  
TGGTTGTTGGACCTGACTTGTTAATGGCTACTGCTTTACTAAGGAGATGTGCAATGCTGAAG  
TTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAG  
GCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACACGGAGAAA  
CCCTATCTCTACTAAAAATACAAAGTAGCCCGGCGTGGTGATGCGTGCCCTGTAATCCCAGCT  
ACCCAGGAAGGCTGAGGCGGCAGAATCACTTGAACCCGAGGCCGAGGTTGCGGTAAGCCGAG  
ATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAAGAAAAGAACACGGTTAATACCATATNA  
ATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGGCTCCTAGTGAT  
TGGTGGCCTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAAATG  
TATCAATATGTTATAGATGAGGTAGAAAGTTATATTTATATTCAATATTTACTTCTTAAGGC  
TAGCGGAATATCCTTCCTGGTTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACA  
TTGTATCATAAGATAAAGTAGTAAACCAGTCTACATTTTCCCATTTCTGTCTCATCAAAAAC  
TGAAGTTAGCTGGGTGTGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGGGCCAAGGAGGG  
TGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTCTA  
CTAAAAATACAAAATTAGCCAGGCGTGGTGGTGCACACCTGTAGTCCCAGCTACTCGGGAG  
GCTGAGACAGGAGATTTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATTGTGCC  
ACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAAAAAAAAGAAGCAGA  
CCTACAGCAGCTACTATTGAATAAATACCTATCCTGGATTTT

**FIGURE 53**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44194

><subunit 1 of 1, 211 aa, 1 stop

><MW: 24172, pI: 5.99, NX(S/T): 1

MRLFLWNAVLTLFVTSLLIGALIPPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGSL  
FHSTHKHNNGQPIWFTLGILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEGKGKIPPEST  
LIFNIDLLEIRNGPRSHESFQEMDLNDDWKLSKDEVKAYLKKEFEKHGAVVNESHHDALVED  
IFDKEDDKDGFISAREFTYKHDEL

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 176-179

**Casein kinase II phosphorylation site.**

amino acids 143-146, 156-159, 178-181 and 200-203

**Endoplasmic reticulum targeting sequence.**

amino acids 208-211

**FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 78-114 and 118-131

**EF-hand calcium-binding domain.**

amino acids 191-203, 184-203 and 140-159

**S-100/ICaBP type calcium binding domain**

amino acids 183-203

54/237

**FIGURE 54**

AATAAAGCTTCCTTAATGTTGTATATGTCTTTGAAGTACATCCGTGCATTTTTTTTTTAGCAT  
CCAACCATTCCTCCCTTGTAAGTCTCGCCCCCTCAAATCACCTCTCCCGTAGCCCAACCGA  
CTAACATCTCAGTCTCTGAAAATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCT  
CACGGGGCTCAGTCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCACAGTAC  
CTGCCACCCTCAACGTCTCAATGGCTCTGACGCCCCGCTGCCCTGCACCTTCAACTCCTGC  
TACACAGTGAACCACAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTC  
TGAGGAGATGTTCCCTCCAGTTCGCGATGAAGATCATTAACTGAAGCTGGAGCGGTTTCAAG  
ACCGCGTGGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTGGTGATGCTGAGAAACGTG  
CAGCCGGAGGATGAGGGGATTTACAACCTGCTACATCATGAACCCCCCTGACCGCCACCGTGG  
CCATGGCAAGATCCATCTGCAGGTCCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGG  
CCGTGATTGTGGGTGCCTCCGTGCGGGGGCTTCTGGCTGTGGTCATCTTGGTGCTGATGGTG  
GTCAAGTGTGTGAGGAGAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGA  
GGAGGGCAAGACGGACGGTGAAGGCAACCCGGATGATGGCGCCAAGTAGTGGGTGGCCGGCC  
CTGCAGCCTCCCGTGTCCCGTCTCCTCCCCCTCTCCGCCCTGTACAGTGACCCTGCCTGCTCG  
CTCTTGGTGTGCTTCCCGTGACCTAGGACCCAGGGCCACCTGGGGCCTCCTGAACCCCCG  
ACTTCGTATCTCCACCCCTGCACCAAGAGTGACCCACTCTCTTCCATCCGAGAAACCTGCCA  
TGCTCTGGGACGTGTGGGCCCTGGGGAGAGGAGAGAAAGGGCTCCACCTGCCAGTCCCTGG  
GGGGAGGCAGGAGGCACATGTGAGGGTCCCCAGAGAGAAGGGAGTGGGTGGGCAGGGGTAGA  
GGAGGGGCCGCTGTACCTGCCAGTGCTTGCTGGCAGTGGCTTCAGAGAGGACCTGGTGG  
GGAGGGAGGGCTTTCCTGTGCTGACAGCGCTCCCTCAGGAGGGCCTTGGCCTGGCACGGCTG  
TGCTCCTCCCCCTGCTCCCAGCCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCCTGA  
AACTTGAGGGGCATGTTAAAGGGATGACTGTGCATTCCAGGGCACTGACGGAAAGCCAGGG  
CTGCAGGCAAAGCTGGACATGTGCCCTGGCCCAGGAGGCCATGTTGGGCCCTCGTTTCCATT  
GCTAGTGGCCTCCTTGGGGCTCCTGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAG  
ACTGGAAGAGCAGCTCCAGGTAGGGGGCCATGTTTCCCAGCGGGGACCCACCAACAGAGGCC  
AGTTTCAAAGTCAGCTGAGGGGCTGAGGGGTGGGGCTCCATGGTGAATGCAGGTTGCTGCAG  
GCTCTGCCTTCTCCATGGGGTAACCACCCTCGCCTGGGCAGGGGCAGCCAAGGCTGGGAAAT  
GAGGAGGCCATGCACAGGGTGGGGCAGCTTCTTTGGGGCTTCAGTGAGAACTCTCCCAGTT  
GCCCTTGGTGGGGTTTCCACCTGGCTTTTGGCTACAGAGAGGGAAGGGAAAGCCTGAGGCCG  
GCATAAGGGGAGGCCTTGGAACCTGAGCTGCCAATGCCAGCCCTGTCCCATCTGCGGCCACG  
CTACTCGCTCCTCTCCCAACAACCTCCCTTCGTGGGGACAAAAGTGACAATTGTAGGCCAGGC  
ACAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCGGGTGGATTACCTCCAT  
CTGTTTAGTAGAAATGGGCAAAACCCCATCTCTACTAAAAATACAAGAATTAGCTGGGCGTG  
GTGGCGTGTGCCTGTAATCCCAGCTATTTGGGAGGCTGAGGCAGGAGAATCGCTTGAGCCCC  
GGAAGCAGAGGTTGCAGTGAACCTGAGATAGTGATAGTGCCACTGCAATTCAGCCTGGGTGAC  
ATAGAGAGACTCCATCTCAAAAAAA

**FIGURE 55**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415

<subunit 1 of 1, 215 aa, 1 stop

<MW: 24326, pI: 6.32, NX(S/T): 4

MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNVLNGSDARLPCTFNSCYTVNHKQ  
FSLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMRLRVQPEDEGI  
YNCYIMNPPDRHRGHGKIHLQVLMEEPPEPDRDSTVAVIVGASVGGFLAVVILVLMVVKCVRRK  
KEQKLSTDDLKTEEEGKTDGEGNPDDGAK

**Important features:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 161-179

**Immunoglobulin-like fold:**

amino acids 83-127

**N-glycosylation sites.**

amino acids 42-45, 66-69 and 74-77

**FIGURE 56**

GTTGTATATGTCCTGAAGTACATCCGTGCATTTTTTTTAGCATCCAACCATCCTCCCTTGTA  
GTTCTCGCCCCCTCAAATCACCTTCTCCCTTAGCCCACCCNACTAACATCTCAGTCTCTGAA  
AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCACGGGGCTCAGTCTCTTTT  
TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCTCAACGTCC  
TCAATGGCTCTGACGCCCCGCTGCCCTGCCCTTCAACTCCTGCTACACAGTGAACCACAAAC  
AGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTCTGAGGAGATGTTCCCTCCAG  
TTCCGCATGAAGATCATTAACTGAAGCTGGAGCGGTTTCAAGACCGCGTGGAGTTCTCAGG  
GAACCCCAGCAAGTACGATGTGTGGTGATGCTGAGAAACGTGCAGCCGGAGGATGAGGGGA  
TTTACAACCTGCTACATCATGAACCCCCC

**FIGURE 57**

TCACGGGGCTCATCTCTTTTCTCTTTGGTGCCCACCAGGACGGAGCATGGAGGTNCACATA  
CCTGCCACCCTCAACGTCCTCAATGGCTTTGACGCCCCGCTGCCCTGCACCTTCAACTCCNG  
CTACACAGTGAACCACAAACAGTTCTCCCTGAACTGGATTTACCAGGAGTGCAACAACCTGGC  
TCTGAGGAGATGTTCTCCAGTTCCCGCATGGAAGATCATTTAACCTGAAAGCTGGAAGCGG  
TTTTCAAGAACCGCGTGGAAGTTTCTCAGGGAACCCAGCAAGTACGATGTGTCGGTGATGC  
TGAGAAACGTGCAGCCGGAGGATGAGGGGATTTACAACTGCTACATCATGAACCCCCC

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**FIGURE 58**

TGCGGCGACCGTCGTACACCATGGGCCTCCACCTCCGCCCCCTACCGTGTGGGGCTGCTCCCG  
GATGGCCTCCTGTTCTCTTGCTGCTGCTAATGCTGCTCGCGGACCCAGCGCTCCCGGCCGG  
ACGTCACCCCCCAGTGGTGCTGGTCCCTGGTGATTTGGGTAACCAACTGGAAGCCAAGCTGG  
ACAAGCCGACAGTGGTGCACTACCTCTGCTCCAAGAAGACCGAAAGCTACTTCACAATCTGG  
CTGAACCTGGAAGTGGTGCTGCTGCCTGTCATCATTGACTGCTGGATTGACAATATCAGGCTGGT  
TTACAACAAAACATCCAGGGGCCACCCAGTTTCTGATGGTGTTGGATGTACGTGTCCCTGGCT  
TTGGGAAGACCTTCTCACTGGAGTTCTGGACCCCAAGCAAAAGCAGCGTGGGTTCTTATTTT  
CACACCATGGTGGAGAGCCTTGTGGGCTGGGGCTACACACGGGGTGAGGATGTCCGAGGGGC  
TCCCTATGACTGGCGCCGAGCCCCAAATGAAAACGGGGCCCTACTTCTGGCCCTCCGCGAGA  
TGATCGAGGAGATGTACCAGCTGTATGGGGGCCCCGTGGTGCTGGTTGCCACAGTATGGGC  
AACATGTACACGCTCTACTTTCTGCAGCGGCAGCCGCAGGCCTGGAAGGACAAGTATATCCG  
GGCCTTCGTGTCACTGGGTGCGCCCTGGGGGGGCGTGGCCAAGACCCTGCGCGTCTGGCTT  
CAGGAGACAACAACCGGATCCCAGTCATCGGGCCCCCTGAAGATCCGGGAGCAGCAGCGGTCA  
GCTGTCTCCACCAGCTGGCTGCTGCCCTACAACATACACATGGTCACCTGAGAAGGTGTTCTGT  
GCAGACACCCACAATCAACTACACACTGCGGGACTACCGCAAGTTCTTCCAGGACATCGGCT  
TTGAAGATGGCTGGCTCATGCGGCAGGACACAGAAGGGCTGGTGGAAGCCACGATGCCACCT  
GGCGTGCACTGCACTGCCTCTATGGTACTGGCGTCCCCACACCAGACTCCTTCTACTATGA  
GAGCTTCCCTGACCGTGACCCTAAAATCTGCTTTGGTGACGGCGATGGTACTGTGAACCTGA  
AGAGTGCCCTGCAGTGCCAGGCCTGGCAGAGCCGCCAGGAGCACCAAGTGTGCTGCAGGAG  
CTGCCAGGCAGCGAGCACATCGAGATGCTGGCCAACGCCACCACCTGGCCTATCTGAAACG  
TGTGCTCCTTGGGCCCTGACTCCTGTGCCACAGGACTCCTGTGGCTCGGCCGTGGACCTGCT  
GTTGGCCTCTGGGGCTGTCATGGCCACGCGTTTTTGCAAAGTTTGTGACTCACCATTCAAGG  
CCCCGAGTCTTGGACTGTGAAGCATCTGCCATGGGGAAGTGCTGTTTGTATCCTTTCTCTG  
TGGCAGTGAAGAAGGAAGAAATGAGAGTCTAGACTCAAGGGACACTGGATGGCAAGAATGCT  
GCTGATGGTGGAAGTGTGTGACCTTAGGACTGGCTCCACAGGGTGGACTGGCTGGGCCCTG  
GTCCCAGTCCCTGCCTGGGGCCATGTGTCCCCCTATTCTGTGGGCTTTTCATACTTGCTTA  
CTGGGCCCTGGCCCCGCGAGCCTTCCTATGAGGGATGTTACTGGGCTGTGGTCTGTACCCAG  
AGGTCCCAGGGATCGGCTCCTGGCCCCCTCGGGTGACCCTTCCCACACACCAGCCACAGATAG  
GCCTGCCACTGGTCATGGGTAGCTAGAGCTGCTGGCTTCCCTGTGGCTTAGCTGGTGGCCAG  
CCTGACTGGCTTCTTGGGCGAGCCTAGTAGCTCCTGCAGGCAGGGGCAGTTTGTGCGTTCT  
TCGTGGTTCCCAGGCCCTGGGACATCTCACTCCACTCCTACCTCCCTTACCACCAGGAGCAT  
TCAAGCTCTGGATTGGGCAGCAGATGTGCCCCCAGTCCCGCAGGCTGTGTTCCAGGGGCCCT  
GATTTCTCGGATGTGCTATTGGCCCCAGGACTGAAGCTGCCTCCCTTACCCTGGGACTGT  
GGTTCCAAGGATGAGAGCAGGGGTTGGAGCCATGGCCTTCTGGGAACCTATGGAGAAAGGGA  
ATCCAAGGAAGCAGCCAAGGCTGCTCGCAGCTTCCCTGAGCTGCACCTCTTGCTAACCCAC  
CATCACACTGCCACCCTGCCCTAGGGTCTCACTAGTACCAAGTGGGTCAGCACAGGGCTGAG  
GATGGGGCTCCTATCCACCCTGGCCAGCACCCAGCTTAGTGCTGGGACTAGCCCAGAACTT  
GAATGGGACCCTGAGAGAGCCAGGGGTCCCCCTGAGGGCCCCCTAGGGGCTTTCTGTCTGCC  
CAGGGTGCTCCATGGATCTCCCTGTGGCAGCAGGCATGGAGAGTCAGGGCTGCCTTCATGGC  
AGTAGGCTCTAAGTGGGTGACTGGCCACAGGCCGAGAAAAGGGTACAGCCTCTAGGTGGGGT  
TCCCAAGACGCCTTCAGGCTGGACTGAGCTGCTCTCCACAGGGTTTCTGTGCAGCTGGAT  
TTTCTCTGTTGCATACATGCCTGGCATCTGTCTCCCCTTGTTCCTGAGTGGCCCCACATGGG  
GCTCTGAGCAGGCTGTATCTGGATTCTGGCAATAAAAGTACTCTGGATGCTGTAAAAAAA  
AAAAAAA



**FIGURE 59**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189

><subunit 1 of 1, 412 aa, 1 stop

><MW: 46658, pI: 6.65, NX(S/T): 4

MGLHLRPFYRVGLLPDGLLELLLLLMLLADPALPAGRHPVVLVPGDLGNQLEAKLDKPTVVH  
YLCSKKTESYFTIWLNLLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGV DVRVPFGKTFSL  
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMI EEMYQ  
LYGGPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNNRI  
PVIGPLKIREQQRSAVSTSWLLPYNYTWSPEKV FVQTPTINYTLRDYRKFFQDIGFEDGWLM  
RQDTEGLVEATMPPGVQLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGT VNLKSALQCO  
AWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLLGP

Important features:

Signal peptide:

amino acids 1-28

Potential lipid substrate binding site:

amino acids 147-164

N-glycosylation sites.

amino acids 99-102, 273-276, 289-292 and 398-401

Lipases, serine proteins

amino acids 189-201

Beta-transducin family Trp-Asp repeat

amino acids 353-365

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**FIGURE 60**

CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCGGG  
GCCTACGGCGCGGCGCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCA  
GGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCCTGCATCTATGGTG  
AGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGAT  
GCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGT  
GGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTG  
ACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTGGTTTCTGCTTCCTCACC AAC  
CAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCGGACTCTGTGAGGGCAGCCAT  
CACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT  
ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACT  
GCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACCTACCAACAGCCACCCTTCACCCAGAA  
CGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAA  
GGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTGCCA  
GCCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC  
TGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCCGCT  
CACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCTCGCTTTTAATGA  
CCTCAGCCCCGCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCT  
CAGCTTCCCCCGGCCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAG  
ACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCA  
CTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGT  
GGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTG  
CTCCACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTC  
TGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTC  
TGTGCCGAGTGTATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACG  
GAATAAATGTTTTCTCATTCAAAG

**FIGURE 61**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48304

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24810, pI: 4.75, NX(S/T): 1

MESGAYGAAGAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEYSNAHESKQMYCVFN  
RNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLIVIGDLLFSALWTFWLVGFC  
FLTNQWAVTNP KDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP  
DPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY

**Important features:**

**Type II Transmembrane domain:**

amino acids 24-43

**Other transmembrane domains:**

amino acids 74-90, 108-126 and 145-161

**N-glycosylation site.**

amino acids 97-100

**FIGURE 62**

GAGCCACCTACCCTGCTCCGAGGCCAGGCCTGCAGGGCCTCATCGGCCAGAGGGTGATCAGT  
GAGCAGAAGGATGCCCCGTGGCCGAGGCCCCCAGGTGGCTGGCGGGCAGGGGGACGGAGGTG  
ATGGCGAGGAAGCGGAGCCAGAGGGGATGTTCAAGGCCTGTGAGGACTCCAAGAGAAAAGCC  
CGGGGCTACCTCCGCCTGGTGCCCCCTGTTTGTGCTGCTGGCCCTGCTCGTGCTGGCTTCGGC  
GGGGGTGCTACTCTGGTATTTCTAGGGTACAAGGCGGAGGTGATGGTCAGCCAGGTGTACT  
CAGGCAGTCTGCGTGTACTCAATCGCCACTTCTCCAGGATCTTACCCGCCGGGAATCTAGT  
GCCTTCCGCAGTGAAACCGCCAAAGCCCCAGAAGATGCTCAAGGAGCTCATCACCAGCACCCG  
CCTGGGAACCTTACTACAACTCCAGCTCCGTCTATTCTTTGGGGAGGGACCCCTCACCTGCT  
TCTTCTGGTTCATTCTCAAATCCCCGAGCACCCGCGGCTGATGCTGAGCCCCGAGGTGGTG  
CAGGCACTGCTGGTGGAGGAGCTGCTGTCCACAGTCAACAGCTCGGCTGCCGTCCCTACAG  
GGCCGAGTACGAAGTGGACCCCGAGGGCCTAGTGATCCTGGAAGCCAGTGTGAAAGACATAG  
CTGCATTGAATTCCACGCTGGGTTGTTACCGCTACAGCTACGTGGGCCAGGGCCAGGTCCCTC  
CGGCTGAAGGGGCTGACCACCTGGCCTCCAGCTGCCTGTGGCACCTGCAGGGCCCCAAGGA  
CCTCATGCTCAAACCTCCGGCTGGAGTGGACGCTGGCAGAGTGCCGGGACCGACTGGCCATGT  
ATGACGTGGCCGGGCCCCCTGGAGAAGAGGCTCATCACCTCGGTGTACGGCTGCAGCCGCCAG  
GAGCCCGTGGTGGAGGTTCTGGCGTGGGGGGCCATCATGGCGGTCTGTGGAAGAAGGGCCT  
GCACAGCTACTACGACCCCTTCGTGCTCTCCGTGCAGCCGGTGGTCTTCCAGGCCTGTGAAG  
TGAACCTGACGCTGGACAACAGGCTCGACTCCCAGGGCGTCTCAGCACCCCGTACTTCCCC  
AGCTACTACTCGCCCCAAACCCACTGCTCCTGGCACCTCACGGTGCCCTCTCTGGACTACGG  
CTTGGCCCTCTGGTTTGATGCCTATGCACTGAGGAGGCAGAAGTATGATTTGCCGTGCACCC  
AGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCCTACGCC  
GAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCAGATCTCCCT  
CACCGGGCCCCGGTGTGCGGGTGCATATGGCTTGTACAACCAGTCGGACCCCTGCCCTGGAG  
AGTTCCTCTGTCTGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGACTGCCCC  
AACGGCCTGGATGAGAGAACTGCGTTTGACAGAGCCACATTCCAGTGCAAAGAGGACAGCAC  
ATGCATCTCACTGCCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCGATGAAG  
AGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACCTTCCAGTGTGAGGACCGGAGCTGC  
GTGAAGAAGCCCAACCCGCACTGTGATGGGCGGCCCCGACTGCAGGGACGGCTCGGATGAGGA  
GCACTGTGACTGTGGCCTCCAGGGCCCCCTCCAGCCGCATTGTTGGTGGAGCTGTGTCTCCG  
AGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTCCGGGTGACACATCTGTGGGGGGGCC  
CTCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCATGGCCTC  
CACGGTGCTGTGGACCGTGTTCCTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTGGAGAGG  
TGTCCTTCAAGGTGAGCCGCCTGCTCCTGCACCCGTACCACGAAGAGGACAGCCATGACTAC  
GACGTGGCGCTGCTGCAGCTCGACCACCCGGTGGTGCGCTCGGCCCGCGTGCGCCCCGTCTG  
CCTGCCCGCGCGCTCCCACTTCTTCGAGCCCGGCCTGCACTGCTGGATTACGGGCTGGGGCG  
CCTTGCGCGAGGGCGGCCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTGATCCCA  
CAGGACCTGTGCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGCCGGCTA  
CCGCAAGGGCAAGAAGGATGCCTGTGAGGGTGAAGTCAAGGTGGTCCGCTGGTGTGCAAGGCAC  
TCAGTGGCCGCTGGTTCTTGGCGGGGCTGGTCAGCTGGGGCCTGGGCTGTGGCCGGCCTAAC  
TACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGTGACCTG  
AGGAACTGCCCCCCTGCAAAGCAGGGGCCACCTCCTGGACTCAGAGAGCCCAGGGCAACTGC  
CAAGCAGGGGGACAAGTATTCTGGCGGGGGGTGGGGGAGAGAGCAGGCCCTGTGGTGGCAGG  
AGGTGGCATCTTGTCTCGTCCCTGATGTCTGCTCCAGTGATGGCAGGAGGATGGAGAAGTGC  
CAGCAGCTGGGGGTCAAGACGTCCCTGAGGACCCAGGCCACACCCAGCCCTTCTGCCTCC  
CAATTCTCTCTCCTCCGTCCCTTCTTCCACTGCTGCCTAATGCAAGGCAGTGGCTCAGCAG  
CAAGAATGCTGGTTCTACATCCCGAGGAGTGTCTGAGGTGCGCCCCACTCTGTACAGAGGCT  
GTTTGGGCAGCCTTGCCCTCCAGAGAGCAGATTCCAGCTTCGGAAGCCCCCTGGTCTAACTTGG  
GATCTGGGAATGGAAGGTGCTCCCATCGGAGGGGACCCCTCAGAGCCCTGGAGACTGCCAGGT  
GGGCCTGCTGCCACTGTAAGCCAAAAGGTGGGGAAGTCTGACTCCAGGGTCTTGCCCCAC  
CCCTGCCTGCCACCTGGGCCCTCACAGCCAGACCTCACTGGGAGGTGAGCTCAGCTGCCC  
TTTGAATAAAGCTGCCTGATCAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 63**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152  
><subunit 1 of 1, 802 aa, 1 stop  
><MW: 88846, pI: 6.41, NX(S/T): 7  
MPVAEAPQVAGGQGDGGDGEAEPEGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL  
LWYFLGYKAEVMVSQVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQKMLKELITSTRLGT  
YINSSSVYSFGEGPLTCFFWFILQIPEHRLMLSPEVVQALLVEELLSTVNSSAAVPYRAEY  
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQGVRLKGPDLHLASSCLWHLQGPDKDLML  
KLRLEWTLAECDRLAMYDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSY  
YDPFVLSVQPVVFQACEVNLTLDNRLDSQGVLSPTYFPSYYSPTHCWSHLTVPSLDYGLAL  
WFDAYALRRQKYDLPCTQGQWTIQNRRLCGLRILQPYAERIPVVATAGITINFTSQISLTGP  
GVRVHYGLYNQSDPCPGEFLCSVNGLCVPACDGVKDCPNGLDERNCVCRATFOCKEDSTCIS  
LPKVCDGQPDCLNGSDEEQCQEGVPCGTFTTFQCEDRSCVKKPNPQCDGRPDGRDGSDEEHCD  
CGLQGPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIADRWVITAHCFOEDSMASSTVL  
WTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALQLDHPVVRSAAVRPVCLPA  
RSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCSEAYRYQVTPRMLCAGYRKG  
KKDACQGDSSGGPLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWQQVVT

**Important features:**

**Type II transmembrane domain:**

amino acids 46-67

**Serine proteases, trypsin family, histidine active site.**

amino acids 604-609

**N-glycosylation sites.**

amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447  
and 509-512

**Kringle domains.**

amino acids 746-758 and 592-609

**Homologous region to Kallikrein Light Chain:**

amino acids 568-779

**Homologous region to Low-density lipoprotein receptor:**

amino acids 451-567

**FIGURE 64**

GCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCC  
TACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCCAGAT  
CTCCCTCACCGGGCCCCGGTGTGCGGGTGCACTATGGCTTGTACAACCAGTCGGACCCCTGCC  
CTGGAGAGTTCCTCTGTTCTGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGAC  
TGCCCCAACGGCCTGGATGAGAGAACTGCGTTTGAGAGCCACATTCCAGTGCAAAGAGGA  
CAGCACATGCATCTCACTGCCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGGCAGCG  
ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACCTTCCAGTGTGAGGACCGG  
AGCTGCGTGAAGAAGCCCAACCCGCAGTGTGATGGGCGGCCCCGACTGCAGGGACGGCTCGGA  
TGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCCTCCAGCCGCATTGTTGGTGGAGCTGTGT  
CCTCCGAGGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTCCGGGGTCGACACATCTGTGGG  
GGGGCCCTCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCAT  
GGCCTCCACGGTGCTGTGGACCGTGTTCTTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTG  
GAGAGGTGTCCTTCAAGGTGAGCCGCTGCTCCTGCACCCGTACACGAAGAGGACAGCCAT  
GACTACGACGTGGCGCTGCTGCAGCTCGACCACCCGGTGGTGCCTCGGCCGCCGTGCGCCC  
CGTCTGCCTGCCCGCGCGCTCCCACTTCTTCGAGCCCGGCCTGCACTGCTGGATTACGGGCT  
GGGGCGCCTTGCGCGAGGGCGGCCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTG  
ATCCACAGGACCTGTGCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGC  
CGGCTACCGCAAGGGCAAGAAGGATGCCTGTCAGGGTGA CT CAGGTGGTCCGCTGGTGTGCA  
AGGCACTCAGTGGCCGCTGGTTCTTGGCGGGGCTGGTCAGCTGGGGCCTGGGCTGTGGCCGG  
CCTAACTACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT  
GACCTGAGGAACTGCCCCCTGCAAAGCAGGGCCACCTCCTGGACTCAGAGAGCCCAGGGC  
AACTGCCAAGCAGGGGGACAAGTAT



**FIGURE 65**

GGACGAGGGCAGATCTCGTTCTGGGGCAAGCCGTTGACACTCGCTCCCTGCCACCGCCCGGG  
CTCCGTGCCGCCAAGTTTTTCATTTTCCACCTTCTCTGCCTCCAGTCCCCCAGCCCCTGGCCG  
AGAGAAGGGTCTTACCGGCCGGGATTGCTGGAAACACCAAGAGGTGGTTTTTTGTTTTTTAAA  
ACTTCTGTTTTCTTGGGAGGGGGTGTGGCGGGGCAGGATGAGCAACTCCGTTCCCTCTGCTCTG  
TTTCTGGAGCCTCTGCTATTGCTTTGCTGCGGGGAGCCCCGTACCTTTTGGTCCAGAGGGAC  
GGCTGGAAGATAAGCTCCACAAACCCAAAGCTACACAGACTGAGGTCAAACCATCTGTGAGG  
TTTAACCTCCGCACCTCCAAGGACCCAGAGCATGAAGGATGCTACCTCTCCGTCGGCCACAG  
CCAGCCCCTTAGAAGACTGCAGTTTCAACATGACAGCTAAAACCTTTTTTCATCATTCACGGAT  
GGACGATGAGCGGTATCTTTGAAAACCTGGCTGCACAAACTCGTGTCAGCCCTGCACACAAGA  
GAGAAAGACGCCAATGTAGTTGTGGTTGACTGGCTCCCCCTGGCCCACCAGCTTTACACGGA  
TGCGGTCAATAATACCAGGGTGGTGGGACACAGCATTGCCAGGATGCTCGACTGGCTGCAGG  
AGAAGGACGATTTTTCTCTCGGGAATGTCCACTTGATCGGCTACAGCCTCGGAGCGCACGTG  
GCCGGGTATGCAGGCAACTTCGTGAAAGGAACGGTGGGCCGAATCACAGGTTTGGATCCTGC  
CGGGCCCATGTTTGAAGGGGCGGACATCCACAAGAGGCTCTCTCCGGACGATGCAGATTTTG  
TGGATGTCCTCCACACCTACACGCGTTCCTTCGGCTTGAGCATTGGTATTCAGATGCCTGTG  
GGCCACATTGACATCTACCCCAATGGGGGTGACTTCCAGCCAGGCTGTGGACTCAACGATGT  
CTTGGGATCAATTGCATATGGAACAATCACAGAGGTGGTAAAATGTGAGCATGAGCGAGCCG  
TCCACCTCTTTGTTGACTCTCTGGTGAATCAGGACAAGCCGAGTTTTTGCCTTCCAGTGCAC  
GACTCCAATCGCTTCAAAAAGGGGATCTGTCTGAGCTGCCGCAAGAACCGTTGTAATAGCAT  
TGGCTACAATGCCAAGAAAATGAGGAACAAGAGGAACAGCAAAATGTACCTAAAACCCGGG  
CAGGCATGCCTTTCAGAGGTAACCTTCAGTCCCTGGAGTGTCCCTGAGGAAGGCCCTTAATA  
CCTCCTTCTTAATACCATGCTGCAGAGCAGGGCACATCCTAGCCCAGGAGAAGTGGCCAGCA  
CAATCCAATCAAATCGTTGCAAATCAGATTACACTGTGCATGTCCTAGGAAAGGGAATCTTT  
ACAAAATAAACAGTGTGGACCCCTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 66**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646

><subunit 1 of 1, 354 aa, 1 stop

><MW: 39362, pI: 8.35, NX(S/T): 2

MSNSVPLLCLFWSLCYCFAAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFNLRRTSKDPEHE  
GCYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVDWL  
PLAHQLYTDAVNNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTV  
GRITGLDPAGPMFEGADIAHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDF  
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDSLVDKPSFAFQCTDSNRFFKKGICLS  
CRKNRCNSIGYNAKKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

**Important features:**

**Signal peptide:**

amino acids 1-16

**Lipases, serine active site.**

amino acids 163-172

**N-glycosylation sites.**

amino acids 80-83 and 136-139

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**FIGURE 67**

CGGACGCGTGGGCGGACGCGTGGGCCTGGGCAAGGGCCGGGGCGCCGGGCGGAGCCACCTCT  
TCCCCCTCCCCCGCTTCCCTGTCGCGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCA  
CCCGGCCGGCCCTGGGGGCTGACAGTCGGCAAAGTTTGGCCCGAAGAGGAAGTGGTCTCAAA  
CCCCGGCAGGTGGCGACCAGGCCAGACCAGGGGCGCTCGCTGCCTGCGGGCGGGCTGTAGGC  
GAGGGCGCGCCCCAGTGCCGAGACCCGGGGCTTCAGGAGCCGGCCCCGGGAGAGAAGAGTGC  
GGCGGCGGACGGAGAAAACAACCTCCAAAGTTGGCGAAAGGCACCGCCCCCTACTCCCGGGCTG  
CCGCCGCTCCCCGCCCCCAGCCCTGGCATCCAGAGTACGGGTGAGCCCCGGGCCATGGAGC  
CCCCCTGGGGAGGCGGCACCAGGGAGCCTGGGCGCCCCGGGGCTCCGCCGCGACCCCATCGGG  
TAGACCACAGAAGCTCCGGGACCCTTCCGGCACCTCTGGACAGCCCAGGATGCTGTTGGCCA  
CCCTCCTCCTCCTCCTCCTTGGAGGCGCTCTGGCCCATCCAGACCGGATTATTTTCCAAAT  
CATGCTTGTGAGGACCCCCCAGCAGTGCTCTTAGAAGTGCAGGGCACCTTACAGAGGCCCCCT  
GGTCCGGGACAGCCGCACCTCCCCTGCCAACTGCACCTGGCTCATCCTGGGCAGCAAGGAAC  
AGACTGTCACCATCAGGTTCCAGAAGCTACACCTGGCCTGTGGCTCAGAGCGCTTAACCCTA  
CGCTCCCCCTCTCCAGCCACTGATCTCCCTGTGTGAGGCACCTCCCAGCCCTCTGCAGCTGCC  
CGGGGGCAACGTCAACCATCACTTACAGCTATGCTGGGGCCAGAGCACCCATGGGGCCAGGGCT  
TCCTGCTCTCCTACAGCCAAGATTGGCTGATGTGCCTGCAGGAAGAGTTTCAGTGCCTGAAC  
CACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCCTGTGGCGATGGCTCTGA  
TGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCCTGACCCCAAGACCCGTCCCCTCCCTGC  
CTTGCAATGTCACCTTGGAGGACTTCTATGGGGTCTTCTCCTCTCCTGGATATACACACCTA  
GCCTCAGTCTCCCACCCCCAGTCCTGCCATTGGCTGCTGGACCCCCATGATGGCCGGCGGCT  
GGCCGTGCGCTTCACAGCCCTGGACTTGGGCTTTGGAGATGCAGTGCATGTGTATGACGGCC  
CTGGGGCCCCCTGAGAGCTCCCGACTACTGCGTAGTCTCACCCACTTCAGCAATGGCAAGGCT  
GTCAGTGTGGAGACACTGTCTGGCCAGGCTGTTGTGTCTACCACACAGTTGCTTGGAGCAA  
TGGTCGTGGCTTCAATGCCACCTACCATGTGCGGGGCTATTGCTTGCCTTGGGACAGACCCT  
GTGGCTTAGGCTCTGGCCTGGGAGCTGGCGAAGGCCTAGGTGAGCGCTGCTACAGTGAGGCA  
CAGCGCTGTGACGGCTCATGGGACTGTGCTGACGGCACAGATGAGGAGGACTGCCCAGGCTG  
CCCACCTGGACACTTCCCCTGTGGGGCTGCTGGCACCTCTGGTGCCACAGCCTGCTACCTGC  
CTGCTGACCGCTGCAACTACCAGACTTTCTGTGCTGATGGAGCAGATGAGAGACGCTGTGCG  
CATTGCCAGCCTGGCAATTTCCGATGCCGGGACGAGAAGTGCGTGTATGAGACGTGGGTGTG  
CGATGGGCAGCCAGACTGTGCGGACGGCAGTGATGAGTGGGACTGCTCCTATGTTCTGCCCC  
GCAAGGTCATTACAGCTGCAGTCATTGGCAGCCTAGTGTGCGGCCTGCTCCTGGTCATCGCC  
CTGGGCTGCACCTGCAAGCTCTATGCCATTGCGACCCAGGAGTACAGCATCTTTGCCCCCCT  
CTCCCGGATGGAGGCTGAGATTGTGCAGCAGCAGGCACCCCTTCCCTACGGGCAGCTCATTG  
CCCAGGGTGCCATCCCACCTGTAGAAGACTTTCCCTACAGAGAATCCTAATGATAACTCAGTG  
CTGGGCAACCTGCGTTCTCTGCTACAGATCTTACGCCAGGATATGACTCCAGGAGGTGGCCC  
AGGTGCCCCGCCGTGCTCAGCGGGGCGCTTGATGCGACGCCTGGTACGCCGTCTCCGCCGCT  
GGGGCTTGCTCCCTCGAACCAACACCCCGGCTCGGGCCTCTGAGGCCAGATCCCAGGTCACA  
CCTTCTGCTGCTCCCCCTTGGAGGCCCTAGATGGTGGCACAGGTCCAGCCCGTGAGGGCGGGGC  
AGTGGGTGGGCAAGATGGGGAGCAGGCACCCCACTGCCCATCAAGGCTCCCCCTCCCATCTG  
CTAGCACGTCTCCAGCCCCCACTACTGTCCCTGAAGCCCCAGGGCCACTGCCCTCACTGCCC  
CTAGAGCCATCACTATTGTCTGGAGTGGTGCAGGCCCTGCGAGGCCGCTGTTGCCCAGCCT  
GGGGCCCCCAGGACCAACCCGGAGCCCCCTGGACCCCAACACAGCAGTCCTGGCCCTGGAAG  
ATGAGGACGATGTGCTACTGGTGGCACTGGCTGAGCCGGGGGTGTGGGTAGCTGAGGCAGAG  
GATGAGCCACTGCTTACCTGAGGGGACCTGGGGGCTCTACTGAGGCCTCTCCCCTGGGGGCT  
CTACTCATAGTGGCACAACTTTTAGAGGTGGGTGAGCCTCCCCTCCACCACTTCCCTTCCCT  
GTCCCTGGATTTTACGGGACTTGGTGGGCTCCCGTTGACCCTATGTAGCTGCTATAAAGTTA  
AGTGTCCCTCAGGCAGGGAGAGGGCTCACAGAGTCTCCTCTGTACGTGGCCATGGCCAGACA  
CCCCAGTCCCTTACCACCACTGCTCCCCACGCCACCACCATTTGGGTGGCTGTTTTTAA  
AAGTAAAGTTCTTAGAGGATCATAGGTCTGGACACTCCATCCTTGCCAAACCTCTACCCAAA  
AGTGGCCTTAAGCACCGGAATGCCAATTAAGTAGAGACCCTCCAGCCCCCAAGGGGAGGATT  
TGGGCAGAACCTGAGGTTTTGCCATCCACAATCCCTCCTACAGGGCCTGGCTCACAAAAGA  
GTGCAACAAATGCTTCTATTCCATAGCTACGGCATTGCTCAGTAAGTTGAGGTCAAAAATAA  
AGGAATCATACATCTC

**FIGURE 68**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631

<subunit 1 of 1, 713 aa, 1 stop

<MW: 76193, pI: 5.42, NX(S/T): 4

MLLATLLLLLLGGALAHDPDRIIFPNHACEDPPAVLLEVQGTLOQLVRDSRTSPANCTWLIL  
GSKEQTVTIRFQKLHLACGSERLTLRSPLQPLISLCEAPPSPLQLPGGNVTITYSYAGARAP  
MGQGFLLSYSQDWLMCLQEEFQCLNHRCVSAVQRCDGVDACGDGSDEAGCSSDPFPGLTTPRP  
VPSLPCNVTLEDFYGVFSSPGYTHLASVSHPQSCHWLLDPHDGRRLAVRFTALDLGFGDAVH  
VYDGPGPPESSRLLRSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGFNATYHVRGYCLP  
WDRPCGLGSGLGAGEGLGERCYSEAQRCDGSWDCADGTDEEDCPGCPPGHFPCGAAGTSGAT  
ACYLPADRCNYQTFCADGADERRCRHCQPGNFRRCRDEKCVYETWVCDGQPCADGSDEWDCS  
YVLPRKVITA AVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSY  
GQLIAQGAIPPVEDFPTENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQRGRLMRRLVR  
RLRRWGLLPRTNTPARASEARSQVTPSAAPLEALDGGTGPAREGGAVGGQDGEQAPPLPIKA  
PLPSASTSPAPTTVPEAPGPLPSLPLEPSLLSGVVQALRGRLPSLGPPGPTRSPPGPHTAV  
LALEDEDDVLLVPLAEPGVWVAEAEDEPLLT

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 442-462

LDL-receptor class A (LDLRA) domain proteins

amino acids 411-431, 152-171, 331-350 and 374-393

**FIGURE 69**

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCTATCGCTTCG  
CAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCA  
GACGCGATGGATAACGTGCAGCCGAAAATAAAACATCGCCCCTTCTGCTTCAGTGTGAAAGG  
CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTTTATCATCGCAC  
AAGCCCCCTGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTCATA  
CTTTTATATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTTGGCCTTTGCTTGATAT  
TATCAACTCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAG  
AAACCACAACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTCTT  
GCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCCAGCGGTCCTTACCAGAAAAA  
GCCTGTGCATGAAAAAAAAAGAAGTTTGTAAATTTTATATTACTTTTGTAGTTTGATACTAAGT  
ATTAAACATATTTCTGTATTCTTCCAAAAAAAAAAAAAAAAAAAA

**FIGURE 70**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645  
><subunit 1 of 1, 152 aa, 1 stop  
><MW: 17170, pI: 9.62, NX(S/T): 1  
MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSMTFFIIAQAPEPYIVITGFEVTVILFFILL  
YVLRLDRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTLTVGGGVFALVTAVCCCLAD  
GALIYRKLLFNPSGPYQKKPVHEKKEVL

**Important features:**

Potential type II transmembrane domain:

amino acids 26-42

Other potential transmembrane domain:

amino acids 44-65, 81-101 and 109-129

Leucine zipper pattern

amino acids 78-99 and 85-106

N-myristoylation site.

amino acids 110-115

Ribonucleotide reductase large subunit protein

amino acids 116-127

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**FIGURE 71**

GGGCGAGAAGTAGGGGAGGGCGTGTTCCGCCGCGGTGGCGGTTGCTATCGTTTTGCAGAACC  
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGA  
TGGATAACGTGCAGCCGAAAATAAAACATCGCCCCTTCTGCTTCAGTGTGAAAGGCCACGTG  
AAGATGCTGCGGCTGGCACTAACTGNGACATCTATGACCTTTTTTATNATCGCACAAGCCCC  
TGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTCATACTTTTAT  
ATGTACTCAGACTTGATCGATTAATGAAGTG GTTATTTTGGCCTTTGCTTGATATTATCAAC  
TCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAGAAACCAC  
AACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTNTTGCCGAC

**FIGURE 72**

CAGCCCCGCGCGCCGGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG  
CTGGGCGCGCCCCCGGGCCCCCGCGTGGGCATGGGCGCACTGGCCCCGGGCGCTGCTGCTGC  
CTCTGCTGGCCCAGTGGCTCCTGCGCGCCGCCCGGAGCTGGCCCCCGCGCCCTTCACGCTG  
CCCCCTCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCACCCCGGGACCCGGGACCCC  
TGCCGAGCGCCACGCCGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGG  
GCGCCGCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTAC  
CTGGAGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG  
TAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT  
CTAGCACATAACGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACG  
GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC  
CAATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATAC  
TTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC  
CTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCC  
CGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGT  
ATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTG  
AAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC  
CATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGG  
AAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAG  
CTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCT  
GAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTCAGC  
CCATGATGGGGGCGGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCATCCACAAAT  
GCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAA  
GAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT  
CCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAG  
CCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGCTTT  
AATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCCCGTGACCCTGAGGTGCTCA  
ATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAA  
CCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCG  
CTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCTGCTCCCAGATGCCTTCTAGATTCAC  
TGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTAA  
AAAAAAACTTCATTCTAA

**FIGURE 73**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493  
><subunit 1 of 1, 518 aa, 1 stop  
><MW: 56180, pI: 5.08, NX(S/T): 2  
MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTPGPGTPAERHADGLAL  
ALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHS  
YIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESENF  
FLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGS  
LVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIVDSGTTLR  
LPQKVFDVAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYLRDENSRSRFR  
ITILPOLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCA  
EIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCGAILLVLLVLLLPERC  
QRRPRDPEVVNDESSLVRHRWK

**Important features:****Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 466-494

**N-glycosylation sites.**

amino acids 170-173 and 366-369

**Leucine zipper pattern.**

amino acids 10-31 and 197-118

**Eukaryotic and viral aspartyl proteases**

amino acids 109-118, 252-261 and 298-310

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**FIGURE 74**

CGCCTCCGCCTTCGGAGGCTGACGCGCCCGGGCGCCGTTCCAGGCCTGTGCAGGGCGGATCG  
GCAGCCGCCTGGCGGCGATCCAGGGCGGTGCGGGGCCTGGGCGGGAGCCGGGAGGCGCGGCC  
GGCATGGAGGCGCTGCTGCTGGGCGCGGGGTTGCTGCTGGGCGCTTACGTGCTTGTCTACTA  
CAACCTGGTGAAGGCCCCGCGGTGCGGGCGCATGGGCAACCTGCGGGGCCGCACGGCCGTGG  
TCACGGGCGCCAACAGCGGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCGCCGGGGAGCG  
CGCGTGGTGGCTGGCCTGCCGCAGCCAGGAGCGCGGGGAGGCGGCTGCCTTCGACCTCCGCCA  
GGAGAGTGGGAACAATGAGGTCATCTTCATGGCCTTGGACTTGGCCAGTCTGGCCTCGGTGC  
GGGCCTTTGCCACTGCCTTTCTGAGCTCTGAGCCACGGTTGGACATCCTCATCCACAATGCC  
GGTATCAGTTCCTGTGGCCGGACCCGTGAGGCGTTTAACTGCTGCTTCGGGTGAACCATAT  
CGGTCCCTTTCTGCTGACACATCTGCTGCTGCCTTGCTGAAGGCATGTGCCCCCTAGCCGCG  
TGGTGGTGGTAGCCTCAGCTGCCCCACTGTCGGGGACGTCTTGACTTCAAACGCCTGGACCGC  
CCAGTGGTGGGCTGGCGGCAGGAGCTGCGGGCATATGCTGACACTAAGCTGGCTAATGTACT  
GTTTGCCCCGGGAGCTCGCCAACCAGCTTGAGGCCACTGGCGTCACCTGCTATGCAGCCCACC  
CAGGGCCTGTGAACTCGGAGCTGTTCTGCGCCATGTTCTTGATGGCTGCGCCCACTTTTG  
CGCCCATTTGGCTTGGCTGGTGTCTCCGGGCACCAAGAGGGGGTGCCAGACACCCCTGTATTG  
TGCTCTACAAGAGGGCATCGAGCCCCTCAGTGGGAGATATTTTGCCAACCTGCCATGTGGAAG  
AGGTGCCTCCAGCTGCCCCGAGACGACCGGGCAGCCCATCGGCTATGGGAGGCCAGCAAGAGG  
CTGGCAGGGCTTGGGCCTGGGGAGGATGCTGAACCCGATGAAGACCCCCAGTCTGAGGACTC  
AGAGGCCCCATCTTCTCTAAGCACCCCCACCCTGAGGAGCCCACAGTTTCTCAACCTTACC  
CCAGCCCTCAGAGCTCACCAGATTTGTCTAAGATGACGCACCGAATTCAGGCTAAAGTTGAG  
CCTGAGATCCAGCTCTCCTAACCTCAGGCCAGGATGCTTGCCATGGCACTTCATGGTCCTT  
GAAAACCTCGGATGTGTGTGAGGCCATGCCCTGGACACTGACGGGTTTGTGATCTTGACCTC  
CGTGGTTACTTTCTGGGGCCCCAAGCTGTGCCCTGGACATCTCTTTTCTGTTGAAGGAAT  
AATGGGTGATTATTTCTTCTGAGAGTGACAGTAACCCAGATGGAGAGATAGGGGTATGCT  
AGACACTGTGCTTCTCGGAAATTTGGATGTAGTATTTTCAGGCCCCACCCTTATTGATTCTG  
ATCAGCTCTGGAGCAGAGGCAGGGAGTTTGCAATGTGATGCACTGCCAACATTGAGAATTAG  
TGAACCTGATCCCTTTGCAACCGTCTAGCTAGGTAGTTAAATTACCCCCATGTTAATGAAGCG  
GAATTAGGCTCCCGAGCTAAGGGACTCGCCTAGGGTCTCACAGTGAGTAGGAGGAGGGCCTG  
GGATCTGAACCCAAGGGTCTGAGGCCAGGGCCGACTGCCGTAAGATGGGTGCTGAGAAGTGA  
GTCAGGGCAGGGCAGCTGGTATCGAGGTGCCCCATGGGAGTAAGGGGACGCCTTCCGGGCGG  
ATGCAGGGCTGGGGTCATCTGTATCTGAAGCCCCTCGGAATAAAGCGCGTTGACCGCCAAA  
AAAAAAAAAAAAAAAA

**FIGURE 75**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48227

<subunit 1 of 1, 377 aa, 1 stop

<MW: 40849, pI: 7.98, NX(S/T): 0

MEALLLGAGLLLGAYVLVYYNLVKAPPCGGMGNLRGRTAVVTGANSIGKMTALELARARGAR  
VVLACRSQERGEAAAFDLRQESGNNEVIFMALDLASLASVRAFATAFLSSEPRLDILIHNAG  
ISSCGRTREAFNLLLRVNHIGPFLLTHLLLPCLKACAPSRVVVVASAAHCRGRDLDFKRLDRP  
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCTYAAHPGPVNSELFLRHVPGWLRPLLR  
PLAWLVLRAPRGGAQTPLYCALQEGIEPLSGRYFANCHVEEVPPAARDRAAHLWEASKRL  
AGLGPGEAEPEDEDPQSEDEAPSSLSTPHPEEPTVSQPYPSPQSSPDLSKMTHRIQAKVEP  
EIQLS

Important features:

Signal peptide:

amino acids 1-16

Glycosaminoglycan attachment site.

amino acids 46-49

Short-chain alcohol dehydrogenase family

amino acids 37-49 and 114-124

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**FIGURE 76A**

GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATGGG  
AGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTCCAGG  
GCCCTGGCCCTGCCAGGATGAGCTGCCAAGCCTCAGGCCAGCCACCTCCCACCATCCGCTGG  
TTGCTGAATGGGCAGCCCCCTGAGCATGGTGCCCCCAGACCCACACCACCTCCTGCCTGATGG  
GACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCACGATGGCCAGGCCCTGTCCA  
CAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGCAGTCAGCAGAGGC  
GCTCGGCTGTCTGTGGCTGTCTCCGGGAGGATTTCCAGATCCAGCCTCGGGACATGGTGGC  
TGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCGCCCTGGGGCCACCCAGAGCCCACAG  
TCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCAGGACACACAGTGTCCGGG  
GGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGGGACCTACATGTGTGTGGCCAC  
CAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCCGGGTTTCCATCCAGGAGCCCCAGGACT  
ACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTTCAGCTGGAAAATGTGACACTGCTGAAC  
CCGGATCCTGCAGAGGGCCCCAAGCCTAGACCGGCGGTGTGGCTCAGCTGGAAGGTCAGTGG  
CCCTGCTGCGCCTGCCCAATCTTACACGGCCTTGTTCAGGACCCAGACTGCCCCGGGAGGCC  
AGGGAGCTCCGTGGGCAGAGGAGCTGCTGGCCGGCTGGCAGAGCGCAGAGCTTGGAGGCCTC  
CACTGGGGCCAAGACTACGAGTTCAAAGTGAGACCATCCTCTGGCCGGGCTCGAGGCCCTGA  
CAGCAACGTGCTGCTCCTGAGGCTGCCGGAAAAAGTGCCCAAGTGCCCCACCTCAGGAAGTGA  
CTCTAAAGCCTGGCAATGGCACTGTCTTTGTGAGCTGGGTCCCACCACCTGCTGAAAACCAC  
AATGGCATCATCCGTGGCTACCAGGTCTGGAGCCTGGGCAACACATCACTGCCACCAGCCAA  
CTGGACTGTAGTTGGTGAGCAGACCCAGCTGGAAATCGCCACCCATATGCCAGGCTCCTACT  
GCGTGCAAGTGGCTGCAGTCACTGGTGTGAGCTGGGGAGCCCAGTAGACCTGTCTGCCTC  
CTTTTAGAGCAGGCCATGGAGCGAGCCACCCAAGAACCAGTGAGCATGGTCCCTGGACCCT  
GGAGCAGCTGAGGGCTACCTTGAAGCGGCCTGAGGTCAATTGCCACCTGCGGTGTTGCACTCT  
GGCTGCTGCTTCTGGGCACCGCGTGTGTATCCACCGCCGGCGCCGAGCTAGGGTGCACCTG  
GGCCCAGGTCTGTACAGATATAACAGTGAGGATGCCATCCTAAAACACAGGATGGATCACAG  
TGAATCCCAGTGGTTGGCAGACACTTGGCGTTCCACCTCTGGCTCTCGGGACCTGAGCAGCA  
GCAGCAGCCTCAGCAGTCGGCTGGGGGCGGATGCCCGGGACCCACTAGACTGTCGTGCTCC  
TTGCTCTCCTGGGACTCCCGAAGCCCCGGCGTGCCCTGCTTCCAGACACCAGCACTTTTA  
TGGCTCCCTCATCGCTGAGCTGCCCTCCAGTACCCAGCCAGGCCAAGTCCCCAGGTCCCAG  
CTGTCAGGCGCCTCCCACCCAGCTGGCCAGCTCTCCAGCCCCCTGTTCCAGCTCAGACAGC  
CTCTGCAGCCGCAGGGGACTCTCTTCTCCCCGCTTGTCTCTGGCCCCCTGCAGAGGCTTGGAA  
GGCCAAAAAGAAGCAGGAGCTGCAGCATGCCAACAGTTCCCCACTGCTCCGGGGCAGCCACT  
CCTTGGAGCTCCGGGCCTGTGAGTTAGGAAATAGAGGTTCCAAGAACCTTTCCCAAAGCCCA  
GGAGCTGTGCCCCAAGCTCTGGTTGCCTGGCGGGCCCTGGGACCGAAACTCCTCAGCTCCTC  
AAATGAGCTGGTTACTCGTCATCTCCCTCCAGCACCCTCTTTCTCATGAAACTCCCCCAA  
CTCAGAGTCAACAGACCCAGCCTCCGGTGGCACCCACAGGCTCCCTCCTCCATCCTGCTGCCA  
GCAGCCCCCATCCCCATCCTTAGCCCCCTGCAGTCCCCCTAGCCCCCAGGCCTCTTCCCTCTC  
TGGCCCCAGCCCAGCTTCCAGTCGCCTGTCCAGCTCCTCACTGTTCATCCCTGGGGGAGGATC  
AAGACAGCGTGCTGACCCCTGAGGAGGTAGCCCTGTGCTTGGAACTCAGTGAGGGTGAGGAG  
ACTCCCAGGAACAGCGTCTCTCCCATGCCAAGGGCTCCTTACACCCCCACCACCTATGGGTA  
CATCAGCGTCCCAACAGCCTCAGAGTTCACGGACATGGGCAGGACTGGAGGAGGGGTGGGGC  
CCAAGGGGGGAGTCTTGCTGTGCCACCTCGGCCCTGCCTCACCCCCACCCCAAGCGAGGGC  
TCCTTAGCCAATGGTTGGGGCTCAGCCTCTGAGGACAATGCCGCCAGCGCCAGAGCCAGCCT  
TGTCAGCTCCTCCGATGGCTCCTTCCCTCGCTGATGCTCACTTTGCCCCGGGCCCTGGCAGTGG  
CTGTGGATAGCTTTGGTTTCGGTCTAGAGCCCAGGGAGGCAGACTGCGTCTTCATAGATGCC  
TCATCACCTCCCTCCCCACGGGATGAGATCTTCCCTGACCCCCAACCTCTCCCTGCCCTGTG  
GGAGTGGAGGCCAGACTGGTTGGAAGACATGGAGGTCAGCCACACCCAGCGGCTGGGAAGGG  
GGATGCCCTCCCTGGCCCCCTGACTCTCAGATCTCTTCCCAGAGAAGTCAGCTCCACTGTCGT  
ATGCCCAAGGCTGGTGCTTCTCCTGTAGATTACTCCTGAACCGTGTCCCTGAGACTTCCCAG  
ACGGGAATCAGAACCCTTCTCCTGTCCACCCACAAGACCTGGGCTGTGGTGTGTGGGTCTT  
GGCCTGTGTTTCTCTGCAGCTGGGGTCCACCTTCCCAAGCCTCCAGAGAGTTCTCCCTCCAC  
GATTGTGAAAACAAATGAAAACAAATTAGAGCAAAGCTGACCTGGAGCCCTCAGGGAGCAA  
AACATCATCTCCACCTGACTCCTAGCCACTGCTTTCTCCTCTGTGCCATCCACTCCCACCAC  
CAGGTTGTTTTGGCCTGAGGAGCAGCCCTGCCTGCTGCTCTTCCCCCACCATTGATCACA



**FIGURE 76B**

GGAAGTGGAGGAGCCAGAGGTGCCTTTGTGGAGGACAGCAGTGGCTGCTGGGAGAGGGCTGT  
GGAGGAAGGAGCTTCTCGGAGCCCCCTCTCAGCCTTACCTGGGCCCCCTCCTCTAGAGAAGAG  
CTCAACTCTCTCCCAACCTCACCATGGAAAGAAAATAATTATGAATGCCACTGAGGCACTGA  
GGCCCTACCTCATGCCAAACAAAGGGTTCAAGGCTGGGTCTAGCGAGGATGCTGAAGGAAGG  
GAGGTATGAGACCGTAGGTCAAAAGCACCATCCTCGTACTGTTGTCACCTATGAGCTTAAGAA  
ATTTGATACCATAAAATGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 77**

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404
<subunit 1 of 1, 985 aa, 1 stop
<MW: 105336, pI: 6.55, NX(S/T): 7
MGGMAQDSPPQILVHPQDQLFQGGPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHLLP
DGTLLLLQPPARGHAHDGQALSTD LGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDM
VAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEGTVMCV
ATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTLLNPDPAEGPKPRPAVWLSWKV
SGPAAPAQSYTALFRTQTAPGGQGAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSGRARG
PDSNVLLRLPEKVPSPAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNTSLPP
ANWTVVGEQTQLEIATHMPGSYCVQVA AVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGFW
TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPGLYRYTSEDAILKHRMD
HSDSQWLADTWRSTSGSRDLSSSSSLSSRLGADARDPLDCRRSLLSWDSRSPGVPLLPDTST
FYGSLIAELPSSTPARPSPQVPAVRRLPPQLAQLSSPCSSSDSLCSRRGLSSPRLSLAPAEA
WKAKKKQELQHANS SPLLRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAWRALGPKLLS
SSNELVTRHLPPAPLFPHETPPTQSQQTQPPVAPQAPSSILLPAAPIPILSPCSPSPQASS
LSGPSPASSRLSSSSSLSSLGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY
GYISVPTASEFTDMGRTGGGVGPKGGVLLCPRPCLTPTPSEGSLANGWGSASEDNAASARA
SLVSSSDGSFLADAHFARALAVAVDSFGFGLEPREADCVFIDASSPPSPRDEIFLTPLNLSLP
LWEWRPDWLEDMEVSHTQRLGRGMPPWPPDSQISSQRSQLHCRMPKAGAS PVDYS

```

**Important features:****Transmembrane domain:**

amino acids 448-467

**N-glycosylation sites:**

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

**N-myristoylation sites.**

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

**Phosphotyrosine interaction domain proteins**

amino acids 740-753

**FIGURE 78**

CTCCCACGGTGTCCAGCGCCCAGAAATGCGGCTTCTGGTCCTGCTATGGGGTTGCCTGCTGCT  
CCCAGGTTATGAAGCCCTGGAGGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT  
CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT  
GGGATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAAT  
GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCTGTGGA  
ACCTCACCCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG  
TCTTTACTGATCTCTCTGTTCTTCCAGGACCCTGCTGTCCTCCCTCCCTTCTCCAC  
CTTCCAGCCTCTGGCTACAACACGCCTGCAGCCCAAGGCAAAAGCTCAGCAAACCCAGCCCC  
CAGGATTGACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG  
GCTGAGGGCCCCCTCCATTGCCAGGGACTTCCCAGTACGGGCACGAAAGGACTTCTCAGTACAC  
AGGAACCTCTCCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCGCCCCCCCCATGCAGC  
TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG  
GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCCTGGTGCTGCTGAGCCTTCTGTCAGC  
CGCAGGCCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA  
CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCACGCTTGACTGCGGAGGAAAAGGAAGCC  
CCTTCCCAGGGCCCCCTGAGGGGGACGTGATCTCGATGCCTCCCTCCACACATCTGAGGAGGA  
GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGT  
GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCACCTCAGCCTCAGAG  
TCCAGCTGCCCCGGACTCCAGGGCTCTCCCCACCCTCCCCAGGCTCTCCTCTTGATGTTCCA  
GCCTGACCTAGAAGCGTTTGTGAGCCCTGGAGCCCAGAGCGGTGGCCTTGCTCTTCCGGCTG  
GAGACTGGGACATCCCTGATAGGTTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCA  
GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACTCCTGGGC  
CTCATGCCCAGTGTGCGGACCCTGCCTTCCCTCCCACTCCAGACCCCCACCTTGTCTTCCCTCCC  
TGGCGTCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGATGAAGAGGAGCATGCT  
GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCT  
GTGAAAAACGTGATTCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG  
GACTCTGAATTCTAACAATGCCAGTGAAGTGTGCACTTGAGTTTGAGGGCCAGTGGGCCCTG  
ATGAACGCTCACACCCCTTCAGCTTAGAGTCTGCATTTGGGCTGTGACGTCTCCACCTGCCC  
CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCCCTGAGGCCTGCTAAG  
TCCAGGCCTTGGTCAGGTCAGGTGCACATTGCAGGATAAGCCCAGGACCGGCACAGAAGTGG  
TTGCCCTTNCCATTTGCCCTCCCTGGNCCATGCCTTCTTGCCCTTTGGAAAAAATGATGAAGA  
AAACCTTGGCTCCTTCCCTTGTCTGGAAAGGGTTACTTGCCTATGGGTTCTGGTGGCTAGAGA  
GAAAAGTAGAAAACCAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG  
ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGCGGGGTGGTGGTAAAGTA  
GCACAACACTACTATTTTTTTTCTTTTTCCATTATTATTGTTTTTTAAGACAGAATCTCGTGCT  
GCTGCCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACTCCGCCTCCTGGGTTCAAGTGATT  
CTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACCACACCTGGCTAATT  
TTTGTACTTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTTGAACCTCCTGAC  
CTCAAATGAGCCTCCTGCTTCAGTCTCCCAAATTGCCGGGATTACAGGCATGAGCCACTGTG  
TCTGGCCCTATTTCTTTTAAAAAGTGAAATTAAGAGTTGTTTCAGTATGCAAACTTGGAAG  
ATGGAGGAGAAAAAGAAAAGGAAGAAAAAATGTCACCCATAGTCTCACCAGAGACTATCAT  
TATTTCTGTTTGTGTTGTTACTTCCCTTCCACTCTTTTCTTCTTACATAATTTGCCGGTGTCTT  
TTTACAGAGCAATTATCTTGTATATACAACCTTGTATCCTGCCTTTTCCACCTTATCGTTCC  
ATCACTTTTATTCAGCACTTCTCTGTGTTTTACAGACCTTTTTTATAAATAAAATGTTTCATCA  
GCTGCATAAAAAAAAAAAAAA

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**FIGURE 79**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196  
<subunit 1 of 1, 332 aa, 1 stop  
<MW: 36143, pI: 5.89, NX(S/T): 1  
MRLLVLLWGCLLLPGYEALLEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS  
GTIYAEEEGQETMKGRVSI RDSRQELSLIVTLWNLTLDAGEYWCGVEKRGPD E SLLISLFV  
FPGPCCPPSPSPPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPG  
TSQYGHERTSQYTGTSPHPATSPPPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI  
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAE E KEAPSQAPEGD  
VISMPPLHTSEEELGFSKFVSA

**Important features:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 248-269

**N-glycosylation site.**

amino acids 96-99

**Fibrinogen beta and gamma chains C-terminal domain.**

amino acids 104-113

**Ig like V-type domain:**

amino acids 13-128

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**FIGURE 80**

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGA  
GCCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTC  
GCTCTGTTGCCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT  
GGACTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAA  
GCCCTGTTTCTTCTCCTTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTCATCCCAA  
AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAAGCCAGGAG  
CAGGGCTCTCAGAAGGCGGTGGTGCCCAAGCTGAGGATCATGTTGTTGGCCCTGGTCTGTCTGC  
TCAGCTGCCTGCTACCCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTG  
CTACATGACTTCGGGCTGGACGGATAACGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGC  
TTATTTTACAAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA  
ACGGGATCTTCCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCCGAACGTCCCAAC  
GTGTGCCGGATGTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC  
CATGAAGATAACCCAAGAGCCTCAGGGTCTGGGTACTGGGAGGCCTGGAGGCATCACTGCC  
AGGGAAAAGACCTCACTGAATGGGTGGATGGCTGTGACTTCTAGGATGGACGGAACCATGCA  
CAGCAGGCTGGGAAATGTGGTTTGGTTCCTGACCTAGGCTTGGGAAGACAAGCCAGCGAATA  
AAGGATGGTTGAACGTGAAA

**FIGURE 81**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52187

<subunit 1 of 1, 146 aa, 1 stop

<MW: 16430, pI: 5.05, NX(S/T): 1

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGLADWVCLAYFTSGFNAAALD  
YEADGSTNNGIFQINSRRWCSNLTPNVPNVCRMYSDDLNPNLKDTVICAMKITQEPQGLGY  
WEAWRHHHCQGKDLTEWVDGCDF

Important features:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 67-72

Homologous region to Alpha-lactalbumin / lysozyme C proteins.

amino acids 34-58 (catalytic domain), 111-132 and 66-107

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**FIGURE 82**

AGCCGCTGCCCCGGGCGGGCGCCCGCGGGCGGCACCAATGAGTCCCCGCTCGTGCCTGCGTTC  
GCTGCGCCTCCTCGTCTTCGCCGTCTTCTCAGCCGCCGCGAGCAACTGGCTGTACCTGGCCA  
AGCTGTCGTCGGTGGGGAGCATCTCAGAGGAGGAGACGTGCGAGAACTCAAGGGCCTGATC  
CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCATGGACTCGGTGCGCCGCGGTGC  
CCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCCGGAACCGGCGCTGGAAGTGTCCACAC  
TCGACTCCTTGCCCGTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCCTTCGTG  
TACGCCATCTCTTCGGCAGGTGTGGCCTTTGCAGTGACGCGGGCGTGCAGCAGTGGGGAGCT  
GGAGAAGTGCGGCTGTGACAGGACAGTGCATGGGGTCAGCCCACAGGGCTTCCAGTGGTCAG  
GATGCTCTGACAACATCGCCTACGGTGTGGCCTTCTCACAGTCGTTTGTGGATGTGCGGGAG  
AGAAGCAAGGGGGCCTCGTCCAGCAGAGCCCTCATGAACCTCCACAACAATGAGGCCGGCAG  
GAAGGCCATCCTGACACACATGCGGGTGAATGCAAGTGCCACGGGGTGTGAGGCTCCTGTG  
AGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCCGCCAGGTGGGTACGCACTGAAGGAG  
AAGTTTGATGGTGCCACTGAGGTGGAGCCACGCCGCGTGGGCTCCTCCAGGGCACTGGTACC  
ACGCAACGCACAGTTCAAGCCGCACACAGATGAGGACCTGGTGTACTTGGAGCCTAGCCCCG  
ACTTCTGTGAGCAGGACATGCGCAGCGGCGTGCTGGGCACGAGGGGCGGCACATGCAACAAG  
ACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGCTGTGGCCGCGGCTTCCACACGGCGCA  
GGTGGAGCTGGCTGAACGCTGCAGCTGCAAATTCCACTGGTGCTGCTTCGTCAAGTGCCGGC  
AGTGCCAGCGGCTCGTGAGTTGCACACGTGCCGATGACCGCCTGCCTAGCCCTGCGCCGGC  
AACCACCTAGTGGCCCAGGGAAGGCCGATAATTTAAACAGTCTCCCACCACCTACCCCAAGA  
GATACTGGTTGTATTTTTTGTCTGGTTTGGTTTTTGGGTCCTCATGTTATTTATTGCCGAA  
ACCAGGCAGGCAACCCCAAGGGCACCAACCAGGGCCTCCCCAAAGCCTGGGCCTTTGTGGCT  
GCCACTGACCAAAGGGACCTTGCTCGTGCCGCTGGCTGCCCCGCATGTGGCTGCCACTGACCA  
CTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGCAGACCTAAGGTGGAGTAACAAGGAGTAT  
TACCACCACATGGCTACTGACCGTGTGATCGGGGAAGAGGGGGCCTTATGGCAGGGAAAATA  
GGTACCGACTTGATGGAAGTCACACCCTCTGGAAAAAAGAACTCTTAACCTCTCCAGCACACA  
TACACATGGACTCCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGG  
GAACAAGCAGATACCAGGTCAAGGGCACCAAGGTTCAATTCAGCCCTTACATGGACAGCTAGA  
GGTTCGATATCTGTGGGTCTTCCAGGCAAGAAGAGGGAGATGAGAGCAAGAGACGACTGAA  
GTCCCACCCTAGAACCCAGCCTGCCCCAGCCTGCCCCCTGGGAAGAGGAACTTAACCACTCC  
CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCCGGCTGTGCCTT  
TGCAGTCATGCCCCGAGTCACCTTTCACAGCGCTGTTCTCCATGAACTGAAAAACACACAC  
ACCTGCGAGA  
GAGAGGGAGGAAAGGGCTGTGCCTTTGCAGTCATGCCCGAGTCACCTTTCACAGCACTGTTCTC

**FIGURE 83**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328

<subunit 1 of 1, 351 aa, 1 stop

<MW: 39052, pI: 8.97, NX(S/T): 2

MSPRSCLRSLRLLVFAVFSAAASNWLYLAKLSSVGSISEEETCEKLKGLIQRQVQMCKRNLE  
VMDSVRRGAQLAIEECQYQFRNRRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSAGVAFV  
TRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYGVAFSOSFVDVRERSKGASSSRALM  
NLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTWCRAVPPFRQVGHALKEKFDGATEVEPRR  
VGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTSKAIDGCELLC  
CGRGFHTAQVELAERCSCKFHWCCFVKCRQCQRLVELHTCR

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation sites.**

amino acids 88-91 and 297-300

**Wnt-1 family signature.**

amino acids 206-215

**Homologous region to Wnt-1 family proteins**

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

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**FIGURE 84**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT  
CGCCATGGACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGC  
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCCTGGTC  
ACCACAGTCCTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGC  
GGCGCTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGGGCGCTGG  
GTGCCCTGAAGGAGGAGGTGCGGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTG  
CAGACCACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCT  
GCGGGAACTGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGGCCGTGAGGACG  
TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACCTCCTGCGAGCCG  
TGCCCCACGTCGTTGGCTGTCCTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGAC  
GTGGGCGGCGGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCC  
TGGATGAGCAGGGCTTCCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCCTGAGG  
GCTGTGCGCCATCTGGGCAAGGTTCAAGGGCTACCAGTGGGTGGACGGAGTCTCTCTCAGCTT  
CAGCCACTGGAACCAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAACTGTGTCATGATGC  
TGCACACGGGGCTGTGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG  
AAAAGGCACAACCTGCTGACCCCCGCCAGTGCCCTGGAGCCGCGCCCATTCAGCATGTCGTA  
TCCTGGGGGCTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTCTTCCT  
CATCCACCGCTGCTGAGTCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCCAGTGCC  
TGGGCTCTGGGACCTCCATGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACCTAACC  
TCCACTAGCTCCAAAATCCCTGCTCCTGCGTCCCCGTGATATGCCTCCACTTCTCTCCCTAA  
CCAAGGTTAGGTGACTGAGGACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAACCTGGA  
AGCTGTTTTTGCAGCCTGAGGAAGCATCAATAAATATTTGAGAAATGAAAAAA

**FIGURE 85**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352

<subunit 1 of 1, 293 aa, 1 stop

<MW: 32562, pI: 6.53, NX(S/T): 2

MDTTRYSKWGGSSSEVPGGPWGRVHWSRRPLEFLALAVLVTTVLWAVILSILLSKASTERAA  
LLDGHDLLRTNASKQTAALGALKEEVGDCHSCCSGTQAQLQTTRAELGEAQAKLMEQESALR  
ELRERVTOGLAEAGRGREDVRTELFRALEAVRLQNNSCPCPTSWLSFEGSCYFFSVPKTTW  
AAAQDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSES  
HWNQGEPCNDWGRENCVMMMLHTGLWNDAPCDSEKDGWICEKRHNC

**Important features:**

**Type II transmembrane domain:**

amino acids 31-54

**N-glycosylation sites.**

amino acids 73-76 and 159-162

**Leucine zipper pattern.**

amino acids 102-123

**N-myristoylation sites.**

amino acids 18-23, 133-138 and 242-247

**C-type lectin domain signature.**

amino acids 264-287

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**FIGURE 86**

GCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTCGCTGGGCAGGGCGAGTTGGGAAAGCG  
GCAGCCCCCGCCGCCCCCGCAGCCCCCTTCTCCTCCTTTCTCCCACGTCCTATCTGCCTCTCG  
CTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAGGAACTGGAGCCTCATTGGCCGGCCCCGG  
GGCGCCGGCCTCGGGCTTAAATAGGAGCTCCGGGCTCTGGCTGGGACCCGACCGCTGCCGGC  
CGCGCTCCCGCTGCTCCTGCCGGGTGATGGAAAACCCAGCCCCGGCCGCCCTGGGCAAG  
GCCCTCTGCGCTCTCCTCCTGGCCACTCTCGGCGCCGCCGGCCAGCCTCTTGGGGGAGAGTC  
CATCTGTTCCGCCAGAGCCCCGGCCAAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGA  
CGGCCTTCCCCAAGCAGTACCCCTGTTCGGCCCCCCTGCGCAGTGGTCTTCGCTGCTGGGG  
GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTCAGTAACGGGCTGCG  
CGACTTTGCGGAGCGCGGCGAGGCCTGGGCGCTGATGAAGGAGATCGAGGCGGCGGGGGAGG  
CGCTGCAGAGCGTGCACGAGGTGTTTTCGGCGCCCGCCGTCCCCAGCGGCACCGGGCAGACG  
TCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGTCTCGTTTGTGGTGCGCATCGTGCC  
CAGCCCCGACTGGTTCTGTGGGCGTGGACAGCCTGGACCTGTGCGACGGGGACCGTTGGCGGG  
AACAGGCGGCGCTGGACCTGTACCCCTACGACGCCGGGACGGACAGCGGCTTCACCTTCTCC  
TCCCCCAACTTCGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCCTCCTCTCCCAG  
CCACCCGGCCAACTCCTTCTACTACCCGCGGCTGAAGGCCCTGCCTCCCATCGCCAGGGTGA  
CACTGCTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCCAGTCCTGCCCAGC  
AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCCAGAAACGCCGCTGGACTGCGAGGTCTC  
CCTGTGGTCGTCTTGGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA  
CTCGCTACGTCCGGGTCCAGCCCGCCAACAACGGGAGCCCCCTGCCCCGAGCTCGAAGAAGAG  
GCTGAGTGCGTCCCTGATAACTGCGTCTAAGACCAGAGCCCCGCAGCCCCCTGGGGCCCCCGG  
GAGCCATGGGGTGTCGGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGGCCGAGGGCACAGGG  
GGTTTCGCGCTGCTCCTGACCGCGGTGAGGCCGCGCCGACCATCTCTGCACTGAAGGGCCCT  
CTGGTGGCCGGCACGGGCATTGGGAAACAGCCTCCTCCTTTCCCAACCTTGCTTCTTAGGGG  
CCCCCGTGTCCCGTCTGCTCTCAGCCTCCTCCTCCTGCAGGATAAAGTCATCCCCAAGGCTC  
CAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGCTGCTCCAGGAGATTGTCCTTCATCG  
TCCAGGGGCTGGCTCCACGTTGGTGCAGATACCTCAGACCTGGTGCTCTAGGCTGTGCTG  
AGCCCACTCTCCCGAGGGCGCATCCAAGCGGGGGCCACTTGAGAAGTGAATAAATGGGGCGG  
TTTCGGAAGCGTCAGTGTTTCCATGTTATGGATCTCTCTGCGTTTGAATAAAGACTATCTCT  
GTTGCTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 87**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53971

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35844, pI: 5.45, NX(S/T): 2

MENPSPAAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPL  
FRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAEERGEAWALMKEIEAAGEALQSVHEVF  
SAPAVPSGTGQTSAELEVQRRHSLVSFVVRIVPSPDWFVGVDSLDLDCDGRWREQAALDLYP  
YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLLRLRQSP  
RAFIPPAPVLPSRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGR LGTKSRTRYVRVQPA  
NNGSPCPELEEEAECVPDNCV

Important features:

Signal peptide:

amino acids 1-26



**FIGURE 88**

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTTTGGTGTCCCTGTCTTGCGTGA  
TATTGACAAACTGAAGCTTTCCTGCACCACTGGACTTAAGGAAGAGTGTA CTCTAGGCGGA  
CAGCTTTAGTGGCCGGCCGGCCGCTCTCATCCCCGTAAGGAGCAGAGTCCTTTGTACTGAC  
CAAGATGAGCAACATCTACATCCAGGAGCCTCCCACGAATGGGAAGGTTTTATTGAAAATA  
CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTGCAGAAATTTT  
ATCCAACCTTTGTTTGGAAAGCTTATTATGACAATACCATTTTTTCATAGAGTTGTGCCTGGTTT  
CATAGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGC  
CATTCAAAGATGAATTTTCATTCACGGTTGCGTTTTTAATCGGAGAGGACTGGTTGCCATGGCA  
AATGCTGGTTCTCATGATAATGGCAGCCAGTTTTTCTTCACACTGGGTCGAGCAGATGAACT  
TAACAATAAGCATACCATCTTTGGAAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC  
TGTCAGAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAAAAGCTGT  
GAGGTTTTGTTTAATCCTTTTGATGACATCATTCGAAGGGAAATTAAAAGGCTGAAAAAGA  
GAAACCAGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAAATTTTAGTTTACTTT  
CATTTGGAGAGGAAGCTGAGGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG  
GGCAAAAGCAAAAGTAGTCATGACTTGCTTAAGGATGATCCACATCTCAGTTCTGTTCCAGT  
TG TAGAAAGTGAAAAAGGTGATGCACCAGATTTAGTTGATGATGGAGAAGATGAAAGTGCAG  
AGCATGATGAATATATTGATGGTGATGAAAAGAACCTGATGAGAGAAAGAATTGCCAAAAAA  
TTAAAAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC  
AGTCAGCCGCAGTGAAGAGCTCAGAAAAGAAGCAAGACAATTAAAACGGGAACCTTTAGCAG  
CAAAACAAAAAAAAGTAGAAAATGCAGCAAAACAAGCAGAAAAAAGAAGTGAAGAGGAAGAA  
GCCCCCTCCAGATGGTGCTGTTGCCGAATACAGAAGAGAAAAGCAAAAGTATGAAGCTTTGAG  
GAAGCAACAGTCAAAGAAGGGAACCTCCCGGGAAGATCAGACCCTTGCACTGCTGAACCAGT  
TTAAATCTAAACTCACTCAAGCAATTGCTGAAACACCTGAAAATGACATTCCTGAAACAGAA  
GTAGAAGATGATGAAGGATGGATGTCACATGTACTTCAGTTTGAGGATAAAAGCAGAAAAGT  
GAAAGATGCAAGCATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGA  
ATAAAAGAAGGAGGGAAGAAAGCAAAAAGCTGATGAGAGAGAAAAAAGAAAGAAGATATAAAT  
GAGAATAATGATAACCAGAACTTGCTGGAAATGTGCCTACAATGGCCTTGTAACAGCCATTG  
TTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTTGAACCTGTTGTCTGGTTTTG  
AAAAACAATTATCTTGTTTTGCAAATTGTGGAATGATGTAAGCAAATGCTTTTGGTTACTGG  
TACATGTGTTTTTTTCCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTCTT  
TCCACAAAAA

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**FIGURE 89**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919  
><subunit 1 of 1, 472 aa, 1 stop  
><MW: 53847, pI: 5.75, NX(S/T): 2  
MSNIYIQEPPTNGKVLLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYDNTIFHRVVPGFI  
VQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELN  
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPHKIKSCEVLFPFDDIIPREIKRLKKEK  
PEEEVKKLKPKGTKNFSLLSFGEEAESEEEVNRVSQSMKGKSKSSHDLKDDPHLSSVPVV  
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKKLKKDTSANVKSAGEGEVEKKS  
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEAEAPPDGAVAEYRREKQKYEALRK  
QQSKKGTSREDQTLALLNQFKSKLTQAIATPNDIPETEVEDDEGWMSHVLQFEDKSRKVK  
DASMQSDTFEIIDPRNPVKNRRREESKKLMREKKERR

**Important features:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 109-112 and 201-204

**Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.**

amino acids 49-66

**Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase**

amino acids 96-140, 49-89 and 22-51

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**FIGURE 90**

CGCCGCCGTTGGGGCTGGAAGTTCCCGCCAGGTCCGTGCCGGGCGAGAGAGATGCTGCCCGG  
CCCGCCTCGGCTTTGAGGCGAGAGAAGTGTCCCAGACCCATTTGCGCTTGCTGACGGCGTCCG  
AGCCCTGGCCAGACATGTCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACC  
GTGGCCGCCGGCGGGGACCAGCACAGGCGGGCGTTTCTCCTTCGGAACGGGAACGTCTAGCAA  
CCCTTCTGTGGGGCTCAATTTTGGAAATCTTGAAGTACTTCAACTCCAGCAACTACATCTG  
CTCCTTCAAGTGGTTTTGGAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTA  
GGAGGAACAAATACAGGTGCCTTGCACACCAAGAGGCCTCAAGTGGTCACCAAATATGGAAC  
CCTGCAAGGAAAACAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTTAGGAGTCCCCT  
TCTCCAGACCTCCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCCGGAGCCCTGGAAA  
GGAATCAGAGATGCTACCACCTACCCGCTGGATGGAGTCTCGCTCTGTGCGCCAGGCTGGAG  
TGCAGTGGCACGATCTCGGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCGAGTCTCCTGC  
CTCAGCCTCTGAGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCTGGGGCCAGCTGGCCTCG  
ATGTACGTCAGCACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCT  
GAACGTGTACGCGCCGGCGCGCGCGCCCGGGGATCCCCAGCTGCCAGTGATGGTCTGGTTCC  
CGGGAGGCGCCTTCATCGTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCCCGC  
GAGAAAGTGGTGCTGGTGTCTTCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGCACGGA  
CGACAGCCACGCGCGCGGGAACCTGGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTGGGTGC  
AGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCCTGTTCCGGCCAGTCGGCG  
GGGGCCATGAGCATCTCAGGACTGATGATGTACCCCTAGCCTCGGGTCTCTTCCATCGGGC  
CATTTCAGAGTGGCACCGCGTTATTCAGACTTTTCATCACTAGTAACCCACTGAAAGTGG  
CCAAGAAGGTTGCCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAACTGC  
CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGATGAGATTCCTCCAAC  
GAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGG  
TGATCCCAGATGACCCTTTGGTGCTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTT  
CTAGGTGTCAACAACCTGGAATTCAATTGGCTCTTGCCTTATAATATCACCAGGAGCAGGT  
ACCACTTGTGGTGGAGGAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAA  
ACCGTATGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCACACTGCAGACTGCTCAC  
TACCACCGAGAAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTACAACAAGGATGAA  
AAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCATGAAGCTCAAGGAGAAGAAGATGGC  
TTTTTGGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGC  
TATGCAGGAAGGAGCCAAAGAGGGGTTTGGCCCCACCATCCAGGCCCTGGGGAGACTAGCCA  
TGGACATACCTGGGGACAAGAGTTCTACCCACCCAGTTTAGAACTGCAGGAGCTCCCTGCT  
GCCTCCAGGCCAAAGCTAGAGCTTTTGCCTGTTGTGTGGGACCTGCACTGCCCTTTCCAGCC  
TGACATCCCATGATGCCCCCTCTACTTCACTGTTGACATCCAGTTAGGCCAGGCCCTGTCAAC  
ACCACACTGTGCTCAGCTCTCCAGCCTCAGGACAACCTCTTTTTTTCCCTTCTTCAAATCCT  
CCCACCTTCAATGTCTCCTTGTGACTCCTTCTTATGGGAGGTCGACCCAGACTGCCACTGC  
CCCTGTCACTGCACCCAGCTTGGCATTACCATCCATCCTGCTCAACCTTGTTCCCTGTCTGT  
TCACATTGGCCTGGAGGCCTAGGGCAGGTTGTGACATGGAGCAAACCTTTTGGTAGTTTGGGA  
TCTTCTCTCCACCCACACTTATCTCCCCAGGGCCACTCCAAAGTCTATACACAGGGGTGG  
TCTCTTCAATAAAGAAGTGTGATTAGAAAAA

**FIGURE 91**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179  
<subunit 1 of 1, 545 aa, 1 stop  
<MW: 58934, pI: 9.45, NX(S/T): 4  
MSTGFSFGSGTLGSTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTSA PSSG  
FGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLOGKQMHVGKTPIQVFLGVFFSRPP  
LGILRFAPPEPPEPWKGIRDATTYPGWSLALSPGWSAVARSRLTATSASRVQASLLPOPLS  
VWGYRCLOESWGQLASMYVSTRERYKWLRFSEDCLYLVYAPARAPGDPQLPVMVWFPGGAF  
IVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIA  
AFGGDPGNVTLEFGQSAGAMSI SGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA  
HLAGCNHNSTQILVNCLRALSGTKVMRVS NKMRFLQLNFQRDPEEIIWSMSPVVDGVVIPDD  
PLVLLTQGKVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMMD  
IVQDATFVYATLQTAHYHRETPMMGICPAGHATTRMKSTCSWILPQEWA

**Important features:****Signal peptide:**

amino acids 1-29

**Carboxylesterases type-B serine active site.**

amino acids 312-327

**Carboxylesterases type-B signature 2.**

amino acids 218-228

**N-glycosylation sites.**

amino acids 318-321, 380-383 and 465-468

**FIGURE 92**

GAGAACAGGCCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGCT  
GCTGTCCTCGCTGCTGGGCGGGTCCCAGGCTATGGATGGGAGATTCTGGATACGAGTGCAGG  
AGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCCTGCTCTTTCTCCTACCCCCGA  
CAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGGTTCAAAGCAGTGAAGTGAACAAC  
CAAGGGTGCTCCTGTGGCCACAAACCACCAGAGTCGAGAGGTGGAAATGAGCACCCGGGGCC  
GATTCAGCTCACTGGGGATCCCGCCAAGGGGAAGTCTCCTTGGTGATCAGAGACGCGCAG  
ATGCAGGATGAGTCACAGTACTTCTTTTCGGGTGGAGAGAGGAAGCTATGTGACATATAATTT  
CATGAACGATGGGTTCTTTCTAAAAGTAACAGTGCTCAGCTTCACGCCCAGACCCCAGGACC  
ACAACACCGACCTCACCTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACC  
GTCCGACTCCGTGTGGCCTATGCCCCCAGAGACCTTGTATCAGCATTTCACGTGACAACAC  
GCCAGCCCTGGAGCCCCAGCCCCAGGGAAATGTCCCATACCTGGAAGCCCCAAAAGGCCAGT  
TCCTGCGGCTCCTCTGTGCTGCTGACAGCCAGCCCCCTGCCACACTGAGCTGGGTCTGCAG  
AACAGAGTCCTCTCCTCGTCCCATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGG  
GGTGAAGGCTGGGGATTGAGGGCGCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGC  
AGCGAGCCCTGGACCTCTCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAA  
GCAAACAGGACAGTCCTGGAAAACCTTGGGAACGGCACGTCTCTCCAGTACTGGAGGGCCA  
AAGCCTGTGCCTGGTCTGTGTGCACACACAGCAGCCCCCAGCCAGGCTGAGCTGGACCCAGA  
GGGGACAGGTTCTGAGCCCCCTCCAGCCCTCAGACCCCGGGGTCTGGAGCTGCCTCGGGTT  
CAAGTGGAGCACGAAGGAGAGTTACCTGCCACGCTCGGCACCCACTGGGCTCCCAGCACGT  
CTCTCTCAGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAG  
CGTTTCTGGGAATCGGCATCACGGCTCTTCTTTTCTCTGCTGGCCCTGATCATCATGAAG  
ATTCTACCGAAGAGACGGACTCAGACAGAAACCCCGAGGCCCAGGTTCTCCCGGCACAGCAC  
GATCCTGGATTACATCAATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAGA  
AAGCCACACCAAACAGTCCTCGGACCCCTCCTCCACCAGGTGCTCCCTCCCCAGAATCAAAG  
AAGAACCAGAAAAAGCAGTATCAGTTGCCAGTTTCCAGAACCCAAATCATCCACTCAAGC  
CCCAGAATCCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCA  
GACCCAGGCCTGAGGCCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAAGTCAAGTTC  
CAATGAGGGTCTCTTAGGCTTTAGGACTGGGACTTCGGCTAGGGAGGAAGGTAGAGTAAGAG  
GTTGAAGATAACAGAGTGCAAAGTTTCTTCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCT  
CTCTCTTTCTCTCTCTTTTAAAAAACATCTGGCCAGGGCACAGTGGCTCACGCCTGTAATC  
CCAGCACTTTGGGAGGTTGAGGTGGGCAGATCGCCTGAGGTGCGGGAGTTTCGAGACCAGCCTG  
GCCAACTTGGTGAAACCCCGTCTCTACTAAAAATAACAAAATTAGCTGGGCATGGTGGCAGG  
CGCCTGTAATCCTACTACTTGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGACGG  
AGGTTGCAGTGAGCCAAGATCACACCATTTGCACGCCAGCCTGGGCAACAAAGCGAGACTCCA  
TCTCAAAAAAAAATCCTCCAAATGGGTGGGTGTCTGTAATCCCAGCACTTTGGGAGGCTA  
AGGTGGGTGGATTGCTTGAGCCCAGGAGTTTCGAGACCAGCCTGGGCAACATGGTGAAACCCC  
ATCTCTACAAAAAATAACAAACATAGCTGGGCTTGGTGGTGTGTGCCTGTAGTCCCAGCTGT  
CAGACATTTAAACCAGAGCAACTCCATCTGGAATAGGAGCTGAATAAAATGAGGCTGAGACC  
TACTGGGCTGCATTCTCAGACAGTGGAGGCATTCTAAGTCACAGGATGAGACAGGAGGTCCG  
TACAAGATACAGGTCATAAAGACTTTGCTGATAAAACAGATTGCAGTAAAGAAGCCAACCAA  
ATCCCACCAAACCAAGTTGGCCACGAGAGTGACCTCTGGTCTGCTCCTCACTGCTACACTCCT  
GACAGCACCATGACAGTTTACAAATGCCATGGCAACATCAGGAAGTTACCCGATATGTCCCA  
AAAGGGGGAGGAATGAATAATCCACCCCTTGTTTAGCAAATAAGCAAGAAATAACCATAAAA  
GTGGGCAACCAGCAGCTCTAGGCGCTGCTCTTGTCTATGGAGTAGCCATTCTTTTGTTCCTT  
TACTTTCTTAATAAACTTGCTTTCACCTTAAAAAAA



**FIGURE 93**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002  
><subunit 1 of 1, 544 aa, 1 stop  
><MW: 60268, pI: 9.53, NX(S/T): 3  
MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFYSYPRQDWTGSTPAYGYWFK  
AVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPKGNCSLVIRDAQMQDESQYFFRVERGS  
YVTYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVIS  
ISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHPWGPRPL  
GLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLNGTSL  
PVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHP  
LGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPR  
FSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKQYQLPSFPEP  
KSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ

**Important features:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 399-418

**N-glycosylation site.**

amino acids 100-103, 297-300 and 306-309

**Immunoglobulins and major histocompatibility complex proteins  
signature.**

amino acids 365-371

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**FIGURE 94**

TGAAGAGTAATAGTTGGAATCAAAAGAGTCAACGCAATGAACTGTTATTTACTGCTGCGTTT  
TATGTTGGGAATTCCCTCTCCTATGGCCTTGTCTTGGAGCAACAGAAAACCTCTCAAACAAAGA  
AAGTCAAGCAGCCAGTGCGATCTCATTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTT  
TTTGTACCAGAGGAAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTTAGA  
CAATGGAAACAATTCTTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA  
TTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTC  
TACATCTTAAGAGCCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA  
GTTTGTTCATCAAAGTTTCGGATATCAATGACAATGAACCAAAATTCCTAGATGAACCTTATG  
AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT  
GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC  
ATATTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCTAAAATGGATAGAGAAC  
TGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG  
TCTGGAACAACAAGTGTATTAATTAACTTTTCAGATGTTAATGACAATAAGCCTATATTTAA  
AGAAAGTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA  
TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTGAAGAGGAT  
GATTCGCAAACATTTGACATTATTACTAATCATGAACTCAAGAAGGAATAGTTATATTAAA  
AAAGAAAGTGGATTTTGGAGCACCAGAACCACTACGGTATTAGAGCAAAGTTAAAACCATC  
ATGTTCCCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCCTTTCATTAAGATCCAG  
GTGGAAGATGTTGATGAGCCTCCTCTTTTCCCTCCTTCCATATTATGTATTTGAAGTTTTGA  
AGAAACCCACAGGGATCATTGTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAAT  
CTCCTATCAGGTATTCTATTACTAGGAGCAAAGTGTTCATATCAATGATAATGGTACAATC  
ACTACAAGTAACTCACTGGATCGTGAAATCAGTGCTTGGTACAACCTAAGTATTACAGCCAC  
AGAAAAATACAATATAGAACAGATCTCTTCGATCCCCTGTATGTGCAAGTTCTTAACATCA  
ATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAGGCTCT  
GGTCAGGTAATTCAGACTATCAGTGCAAGTGGATAGAGATGAATCCATAGAAGAGCACCATT  
TACTTTAATCTATCTGTAGAAGACACTAACAATTCAAGTTTTACAATCATAGATAATCAAG  
ATAACACAGCTGTCAATTTGACTAATAGAACTGGTTTTAACCTTCAAGAAGAACCTGTCTTC  
TACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACAAACACCCTTAC  
CATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG  
TGCTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTGTCATTATGATCATA  
TTTGGGTTTATTTTTTTGACTTTGGGTTTAAAACAACGGAGAAAACAGATTCTATTTCTGA  
GAAAAGTGAAGATTTGAGAGAGAAATATATTCCAATATGATGATGAAGGGGGTGGAGAAGAAG  
ATACAGAGGCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAACGCAAGACT  
CGGAAAACCAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTTGGCCCCGA  
CAGTGCCATATTCAGGAAATTCATTCTGGAAAAGCTCGAAGAAGCTAATACTGATCCGTGTG  
CCCCCTCTTTTGATTCCCTCCAGACCTACGCTTTTGAGGGGAACAGGGTCATTAGCTGGATCC  
CTGAGCTCCTTAGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT  
GGGACCTCGCTTTAAAAGATTAGCATGCATGTTTGGTTCTGCAGTGCAGTCAAATAATTAGG  
GCTTTTACCATCAAATTTTTTAAAGTGCTAATGTGTATTTCGAACCCAATGGTAGTCTTAA  
AGAGTTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGATTTCC  
CTGGAGTAAATACTCCATGGTTATTTTAAAGCTACCTACATGCTGTCATTGAACAGAGATGTG  
GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATACAACCAGATTTGAAGTAAATAATG  
TAGGAAGATATTAAGTAGATGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATAT  
CATTATTTACTTAGGAAAGAGTAAAAATACCAAACGAGAAAATTTAAAGGAGCAAAAATTTG  
CAAGTCAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAA  
ATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATTCATGAAGTATTGTTTCTTTAT  
TTAA

**FIGURE 95**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906

><subunit 1 of 1, 772 aa, 1 stop

><MW: 87002, pI: 4.64, NX(S/T): 8

MNCYLLLRFMLGIPLLWPCLGATENSQTKKVQPVRSHLRVKRGWVWNQFFVPEEMNTTSHH  
IGQLRSDLDNGNNSFOYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT  
GRAVEPESEFVIKVSNDINDNEPKFLDEPYEAIVPMSPEGTLVIQVTASDADDPSSGNNARL  
LYSLLOGQPYFSVEPTTGVIIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLS  
VNDNKPIFKESLYRLTVSESAPTGTSGTITMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE  
TQEGIVILKKKVD FEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL  
PYYVFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNNINDNGTITTSNSLDREISA  
WYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDR  
DESIEEHFFYFNLSVEDTNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIP  
SLTSTNTLTIHVCDGDSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQ  
RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY  
RQSLQVGPDSAI FRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLES AVSDQD  
ESYDYLNELGPRFKRLACMFGSAVQSNN

**Important features:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 597-617

**N-glycosylation sites.**

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,  
516-519 and 534-537

**Cadherins extracellular repeated domain signature.**

amino acids 136-146 and 244-254

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**FIGURE 96**

ATTTCAAGGCCAGCCATATTTTNTGTTGAACCAACAACAGGAGTCATAAGAATATTTNTA  
AAATGGATAGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGT  
CAGCCAGGAGCGTTGTNTGGAACAACAAGTGTATTAATTAACTTTCAGATGTTAATGACAA  
TAAGCCTATATTTAAAGAAAGTTTATACCGCTTGACTGTNTNTGAATCTGCACCCACTGGGA  
NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC  
AGCATTGAAGAGGATGATTCGCAAACATTTGACATTATT

**FIGURE 97**

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCCGCCCCGGGCGCGGACCCCAACCCCGAC  
CCAGAGCTTCTCCAGCGGGCGGCGCAGCGAGCAGGGCTCCCCGCCTTAACCTCCTCCGCGGGG  
CCCAGCCACCTTCGGGAGTCCGGGTTGCCCACCTGCAAACCTCTCCGCCTTCTGCACCTGCCA  
CCCCTGAGCCAGCGCGGGGCCCCCGAGCGAGTCATGGCCAACGCGGGGCTGCAGCTGTTGGGC  
TTCATTCTCGCCTTCCTGGGATGGATCGGCGCCATCGTCAGCACTGCCCTGCCCCAGTGGAG  
GATTTACTCCTATGCCGGCGACAACATCGTGACCGCCCAGGCCATGTACGAGGGGCTGTGGA  
TGTCCTGCGTGTGCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAAT  
CTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGAT  
AGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGC  
AGAAGATGAGGATGGCTGTCAATTGGGGGTGCGATATTTCTTCTTGCAAGGTCTGGCTATTTTA  
GTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCCCACT  
CAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCC  
TTCTGGGAGGTGCCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCAACACCA  
AGGCCCTATCCAAAACCTGCACCTTCCAGCGGGAAAGACTACGTGTGACACAGAGGCCAAAAG  
GAGAAAATCATGTTGAAACAAACCGAAAAATGGACATTGAGATACTATCATTAACATTAGGAC  
CTTAGAATTTTGGGTATTGTAATCTGAAGTATGGTATTACAAAACAAACAAACAAACAAAA  
ACCCATGTGTTAAATACTCAGTGCTAAACATGGCTTAATCTTATTTTATCTTCTTTCTCTCA  
ATATAGGAGGGAAGATTTTTCATTGTATTACTGCTTCCCATTTGAGTAATCATACTCAAAT  
GGGGGAAGGGGTGCTCCTTAAATATATATAGATATGTATATATACATGTTTTTCTATTAAAA  
ATAGACAGTAAATACTATTCTCATTATGTTGATACTAGCATACTTAAATATCTCTAAAT  
AGGTAAATGTATTTAATTCATATTGATGAAGATGTTTATTGGTATATTTTCTTTTTCGTCC  
TTATATACATATGTAAACAGTCAAATATCATTTACTCTTCTTCATTAGCTTTGGGTGCCTTTG  
CCACAAGACCTAGCCTAATTTACCAAGGATGAATTCCTTCAATTCTTCATGCGTGCCCTTTT  
CATATACTTATTTTATTTTTTACCATAATCTTATAGCACTTGCATCGTTATTAAGCCCTTAT  
TTGTTTTGTGTTTCATTGGTCTCTATCTCCTGAATCTAACACATTTTCATAGCCTACATTTTA  
GTTTCTAAAGCCAAGAAGAATTTATTACAAATCAGAACTTTGGAGGCAAATCTTTCTGCATG  
ACCAAAGTGATAAATTCCTGTTGACCTTCCACACAATCCCTGTACTCTGACCCATAGCACT  
CTTGTTTGCTTTGAAAATATTTGTCCAATTGAGTAGCTGCATGCTGTTCCCCCAGGTGTTGT  
AACACAACCTTTATTGATTGAATTTTAAAGCTACTTATTCATAGTTTTATATCCCCCTAACT  
ACCTTTTTGTTCCTTCCCTTAATTGTATTGTTTTCCCAAGTGTAATTATCATGCGTTTTTA  
TATCTTCCTAATAAGGTGTGGTCTGTTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATA  
ATCTGGTGACAAATATCTCTCTGTAGCTGTAAGCAAGTCACTTAATCTTTCTACCTCTTTT  
TTCTATCTGCCAAATTGAGATAATGATACTTAACCAGTTAGAAGAGGTAGTGTGAATATTAA  
TTAGTTTATATTACTCTTATTCTTTGAACATGAACATATGCCTATGTAGTGTCTTTATTGCT  
CAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAAACCTACACACGTACCTTCATGTGATT  
CACTGCCTTCCTCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACACACATACCTTCAT  
GTGGTTCAGTGCCCTTCCTCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACGCACATAC  
CTTCATGTGGCTCAGTGCCCTTCCTCTCTCTACCAGTCTATTTCCATTCTTTTCAGCTGTGTCT  
GACATGTTTGTGCTCTGTTCCATTTTAAACAACTGCTCTTACTTTTCCAGTCTGTACAGAATG  
CTATTTCACTTGAGCAAGATGATGTAATGGAAAGGGTGTGGCACTGGTGTCTGGAGACCTG  
GATTTGAGTCTTGGTGCTATCAATCACCGTCTGTGTTTGGAGCAAGGCATTTGGCTGCTGTAA  
GCTTATTGCTTCATCTGTAAGCGGTGGTTTGTAAATTCCTGATCTTCCACCTCACAGTGATG  
TTGTGGGGATCCAGTGAGATAGAATACATGTAAGTGTGGTTTTGTAAATTTAAAAAGTGCTAT  
ACTAAGGGAAAGAATTGAGGAATTAACCTGCATACGTTTTGGTGTGCTTTTCAAATGTTTGA  
AAATAAAAAAATGTTAAG

**FIGURE 98**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185

><subunit 1 of 1, 211 aa, 1 stop

><MW: 22744, pI: 8.51, NX(S/T): 1

MANAGLQLLGFILAFILGWIGAIIVSTALPQWRIYSYAGDNIVTAQAMYEGWLWMSCVSQSTGQI  
QCKVFDSLNLSSSTLQATRALMVVGILLGVIAIFVATVGMKCMKCLEDDEVQKMRMAVIGGA  
IFLLAGLAILVATAWYGNRIVQEFYDPMTPVNRARYEFGQALFTGWAAASLCLLGGALLCCSC  
PRKTTSYPTPRPYPKPAPSSGKDYV

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-102, 118-142 and 161-187

N-glycosylation site.

amino acids 72-75

PMP-22 / EMP / MP20 family proteins

amino acids 70-111

ABC-2 type transport system integral membrane protein

amino acids 119-133

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**FIGURE 99**

TTCTGGCCAAACCCGGGGCTNCAGCTGTTGGGCTTCATCTCGCCTTCCTGGGATGGATCGGC  
GCCATCNTCACACTGCCCTTCCCCAGTGGAGGATTTTACTCCCTATGCTGGCGACAACATCG  
TGACCGCCCAGCCCATGTACGAGGGGCTGTGGATGTCCNGCGTGTGCGAGAGCACCGGGCAG  
ATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCCGTGC  
CTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGA  
AGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGC  
GCGATATTTCTTCTTGCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAAN  
CNTTCAACANTTCTATGACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCA  
GGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCT  
GTTCCCTGTCCC

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**FIGURE 100**

ACCCTTGACCCAACGCGGCCCCCGACCGNTTCATGGCCAAACGCGGGNCTCCAGCTGTTGG  
GCTTCATTCTCCCCTTCCTGGGATGGACCGGCGCCCATCNTCAGCACTGCCCTGCCCCAGTG  
GAGGATTTACTCCTATNCCGGCNACAACATCGTGACCGCCCAGGCCNTGTACGAGGGGCTGT  
GGATGTCCTGCGTGTCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCCTTGCT  
GAATCTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAG  
TGATAGCAATCTTNNTGGCCACCGTTGTNNNTGAAGTGTATGAAGTGCTTGGAAGACGATGA  
GGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAGGTCTGGCTA  
TTTtagTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCGA

**FIGURE 101**

GGGCCCCGACCATTTATCCAACCGGGNTCACTGTTGGCTCATCTCCCTCCTGGATGAANCGCGC  
CATCNTCAGACTCCCTGCCCCATGGAGATTTNNCCTATGCTGGCGACAACATCNTGACCCCC  
AGCCATGTACGAGGGGGCTTTGAACGTCNGCGTGTGCGAGANCACCGGGCAGATCCAGTGCAA  
AGTCTTTGACTCCTTGCTGAATCTGNGCAGCACATTGCAGCAACCCNTGCCCTGATGGTGGT  
TGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGT  
GCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTT  
CTTGCAGGTCTGGCTATTTNNNGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAT  
TCTATGACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGC  
TGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCCCTGCGA

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**FIGURE 102**

ATTCTCCCCTCCTGGATGGATCGCNCCACCGTCACATTGCCTTCCCCCANTGGAGGATTNAC  
TCCTATGCTGGCGACAACATCGTGACCCCCCAGGCCATTTACCGAGGGGCTTTGGATGTCNT  
GCNTGTCGCAGAGCACCGGGCAGATCCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAG  
CAGCACATTGCAAGCAACCCGTGCCTTGATGGGGTTGGCATCCTCCTGGGAGTGATAGCAAC  
CTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGCCAGAAG  
ATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTGTTGCAGGTCTGGCTATTTTAGTNGC  
CACAGCATGGTATGGCAATAGANTNNTTCNNGNNNTCTATGACCCTATGACCCCAGTCAATG  
CCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTG  
GGAGGTGCCCTACTTTGCTGTTCTCTGTCCC

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**FIGURE 103**

AGAGCACCGGCAGATCCCAGTNCAAAGTCTTTGACCCTTGCTGAATCTGAGCAGCACATTNC  
AAGCAACCCCTTGCCTTGAAGGTGGTTGNCATCCCCCCTGGGAGTGAATAGCAATCTTTGTG  
GCCACCGTTGGCATGAAGTNTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGAT  
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGACAGGTCTGGCTATTTTAGTNNCCACAGCAT  
GGTATGGCAATAGNATNNTTCGNGGNTTCTATGACCCTATGACCCCAGTCAATGCCAGGTAC  
GAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGC  
CCTACTTTGCTGTTCCCTGTCCCCGAA

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**FIGURE 104**

AGCAATGCCCTGCCCCCAGTGGAGGATTAATTCCTATGNTGGGGACAACATTGTGACNGCCC  
AGGCCATGTACGGGGGGGCTGTGGATGTCCTGCGTGTCGCAGAGCACCGGGCAGATCCAGTGC  
AAAGTNTTTGACTCCTTGCTGAATTTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGT  
GGTTGGCATCTTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTGGNAATGAAGTGTATGA  
AGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTT  
CTTNTTGCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAATNGTTCAAGA  
ATTTTATGACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTTTNTTCACTG  
GCTGGGCTGCTGCTTNTTCTGCCTTNTGGGAGGTGCCCTANTTTGCTGTTTCCTGCGAACC

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**FIGURE 105**

TCATAGGGGGGCGCGATATTTTTCTTGCAGGTNTGGTTATTTTAGTTGCCACAGCATGGTA  
TGGCAATAGAATCGTTCAAGAATTNTATGACCCTATGACCCCAGTCAATGCCAGGTACGAAT  
TTGGTCAGGCTCTNTTCACTGGNTGGGCTGCTGCTTCTNTNNGCCTTNTGGGAGGTGCCCTA  
CTTTGCTGTTTCCTG

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**FIGURE 106**

TTCCTGGGATGGATCCGCCCCATCNTCACATGCCCTGCCCCNTGGAGATTTACNCCTATGC  
TGGCGAACAACATCNTGACCGCCCAGGCCATGTACGAGGGGCTGTGGAATGTCCTGCGTGTC  
CCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACAT  
TGCAAGCAACCNTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGG  
CCACCGTTGGCATGAAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGAT  
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGNNGCCACAGCAT  
GGTATGGCAATCAGACCCNNTCANAACTCTATGACCCTATGACCCCAGTCAATGCCAGGTA  
CGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTG  
CCCTACTTTGCTGTTCCTGTCCCCGAAAAACAACCTCTTACCCACG

**FIGURE 107**

CGGGGCTGCAGCTGTTGGGCTTCATCTCGCTTCCTGGGATGGAATCGGCGCCATCGTCAGCA  
CTGCCCTGCCCCATGGAGGATTTACTCNTATGCTGGCGACAACATCGTGACCNCCCAGGCCA  
TGTACGAGGGGCTGTGGATGTCNGCGTGTCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCT  
TTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCNTGCCTTGATGGTGGTTGGCA  
TCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTG  
GAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTCTTGC  
AGGTCTGGCTATTTNTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTAT  
GACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGC  
TGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCCCTGCGAA

**FIGURE 108**

GCGTGCCGTCAGCTCGCCGGGCACCGCGGCCTCGCCCTCGCCCTCCGCCCCCTGCGCCTGCAC  
CGCGTAGACCGACCCCCCCCCCTCCAGCGCGCCCCACCCGGTAGAGGACCCCCGCCCCGTGCCCCG  
ACCGGTCCCCGCCTTTTTGTAAACTTAAAGCGGGCGCAGCATTAAACGCTTCCCGCCCCGGT  
GACCTCTCAGGGGTCTCCCCGCCAAAGGTGCTCCGCCGCTAAGGAACATGGCGAAGGTGGAG  
CAGGTCTTGAGCCTCGAGCCGCAGCACGAGCTCAAATTCGAGGTCCCTTCACCGATGTTGT  
CACCACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTTAAGGTGAAGACTA  
CAGCACCACGTAGGTACTGTGTGAGGCCAACAGCGGAATCATCGATGCAGGGGCCCTCAATT  
AATGTATCTGTGATGTTACAGCCTTTTCGATTATGATCCCAATGAGAAAAGTAAACACAAGTT  
TATGGTTCAGTCTATGTTTGCTCCAACCTGACACTTCAGATATGGAAGCAGTATGGAAGGAGG  
CAAAACCGGAAGACCTTATGGATTCAAAACTTAGATGTGTGTTTGAATTGCCAGCAGAGAAT  
GATAAACACATGATGTAGAAATAAATAAAATTATATCCACAACCTGCATCAAAGACAGAAAC  
ACCAATAGTGTCTAAGTCTCTGAGTTCTTCTTTGGATGACACCGAAGTTAAGAAGGTTATGG  
AAGAATGTAAGAGGCTGCAAGGTGAAGTTCAGAGGCTACGGGAGGAGACAAGCAGTTCAAG  
GAAGAAGATGGACTGCGGATGAGGAAGACAGTGCAGAGCAACAGCCCCATTTTCAGCATTAGC  
CCCAACTGGGAAGGAAGAAGGCCCTTAGCACCCGGCTCTTGGCTCTGGTGGTTTTGTTCTTTA  
TCGTTGGTGTAATTATTGGGAAGATTGCCTTGTAGAGGTAGCATGCACAGGATGGTAAATTG  
GATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTAAAAAGAAATT  
AATGTATGATGACATCTCACAGGTCTTGCCTTTAAATTACCCCTCCCTGCACACACATACAC  
AGATACACACACACAAATATAATGTAACGATCTTTTAGAAAGTTAAAAATGTATAGTAACTG  
ATTGAGGGGGAAAAAGAATGATCTTTATTAATGACAAGGGAAACCATGAGTAATGCCACAAT  
GGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGCTGGATTACCTC  
TCTTAAATGACACCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTGGAGCCCAGCAT  
GCTGGGGAGTGCGGTGAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCCAGGCTG  
CTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGA  
AGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGT  
TGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACCTAAAGGGACCAA  
GCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACCTGTTATTCAGAGATGTTTAATGCATA  
TTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCAAGAGTACAGTTAATGC  
TGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTGTGGGCTCCTCT  
GTCTCTGGAGAGTCTGGTTCATGTGGAGGTGGGGTTTTATTGGGATGCTGGAGAAGAGCTGCCA  
GGAAGTGTTTTTTCTGGGTGAGTAAATAACAACCTGTCATAGGGAGGGAAATTCTCAGTAGTG  
ACAGTCAACTCTAGGTTACCTTTTTTAATGAAGAGTAGTCAGTCTTCTAGATTGTTCTTATA  
CCACCTCTCAACCATTAACCTCACACTTCCAGCGCCCAGGTCCAAGTCTGAGCCTGACCTCCCC  
TTGGGGACCTAGCCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAAGCGAGGGC  
ACCAGCAGTTGTGGGTGGGGAGCAAGGGAAGAGAGAACTCTTCAGCGAATCCTTCTAGTAC  
TAGTTGAGAGTTTGAAGTGTGAATTAATTTTATGCCATAAAAGACCAACCCAGTTCTGTTTGA  
CTATGTAGCATCTTGAAAAGAAAAATTATAATAAAGCCCCAAAATTAAGAAAA

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**FIGURE 109**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977

<subunit 1 of 1, 243 aa, 1 stop

<MW: 27228, pI: 7.43, NX(S/T): 2

MAKVEQVLSLEPQHELKFRGPFTDVVTNLKLGNPDRNVCFKVKTTAPRRYCVRPNSGIID  
AGASINVSVMLQPFDYDPNEKSKHKEMVQSMFAPTDTSMEAVWKEAKPEDLMDSKLRCVFE  
LPAENDKPHDVEINKIISTTASKTETPIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREE  
NKQFKEEDGLRMRKTVQSNSPISALAPTGKEEGLSTRLLALVVLFFIVGVIIGKIAL

Important features:

Putative transmembrane domain:

amino acids 224-239

N-glycosylation site.

amino acids 68-71

N-myristoylation site.

amino acids 59-64, 64-69 and 235-240

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**FIGURE 110**

GTCAGTCTTCTAGATTGTCCTTATCCCACCTTTCAACCANTACTCACATTTTCNAGCGCCCAG  
GTCCANGTCTGAGCCTGACTTCCCCTTGGGGACCTAGCCTGGAGTCAGGACAATGGNTCGGG  
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTTTGGGTGGGGAGCAAGGGNNGAGAGAAA  
CTCTTCAGCGAATCCTTCTAGTACTAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATA  
AAAGACNAACCCAGTTCTGTTTGACTATGTAGCATCTTGAAAAGAAAAATTATAATAAGCC  
CCAAAATTAAGAATTCTTTTGTCAATTTGTACATTTGCTCTATGGGGGGAATTATTATTTT  
ATCATTTTTATTATTTTGCCATTGGAAGGTAACTTTAAAATGAGC

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**FIGURE 111**

TATTGTAAAGGCCATTTTAAACCATTGGTAGGCCTTGGTACATGATGCTGGATTACCTCCTT  
AAATGACACCNTTCCTCGCCTGTTGGTGCTGGCCNTTGGGGAGCTGGAGCCCCAGCATGCTG  
GGGAGTGCGGTCAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGGCCCAGGCTGCTTT  
CCGTGTCCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCC  
CAAAGGAATTGCCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGTTGA  
CTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCT  
AAATTGTATTGGTTCATGTAGTGAAGTCAAACGTGTTATTCAGAGATGTTTAATGCATATTTA  
ACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAATGCTGCG  
TGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTG

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**FIGURE 112**

CCCTGGTGGTTTTGTTCTTTAATTCGTTGGTGTAATTNTTGGGAAGATTGCTTGTAGAGGTA  
GNATGCACCNGGCTGGTAAATTGGATTGGTGGATCCACCATATCCATGGGATTAAATTTAT  
CATAACCATGTGTAAAAAGAAATTAATGTATGATGACATNTCACAGGTATTGCCTTTAAATT  
ACCCATCCCTGNANACACATACACAGATACACANANACAAATNTAATGTAACGATNTTTTAG  
AAAGTTAAAAATGTATAGTAAC

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**FIGURE 113**

GGTGGCCCATTCCTCGGCCAGGCTGCTTTCGGTNTTCAGTTCTGTCCAAGCCATCAGCTCC  
TTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATNAGACGTAC  
TTGTNATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGT  
GCTTTGTTTCANTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAAGT  
TTATTCAGAGATGTTTAATGCATATTTAANTTATTTAATGTATTTNATNTCATGTTTTCTTA  
TTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAANTNTGTTGGGTGAACTGGTATTGC  
TGCTGGAGGGCTGTGGGCTCCTCTGTCTTTGGAGAGTCTGGTCATGTGGAGGTGGG

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**FIGURE 114**

TGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTTGATGAACAGAGTC  
AGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTG  
TGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGAC  
CAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAAGTGTATTTCAGAGATGTTTAATGC  
ATATTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAA  
TGCTGCGTGC

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**FIGURE 115**

AAACCTTTAAAAGTTGAGGGGAAAAGAATGATCCTTTATTAATGACAAGGGAAACCNTGNGT  
AATGCCACAATGGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGC  
TGGATTACCTCTCTTAAAATGACACCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTN  
GAGCCCAGCATGCTGGGGAGTGCGGTCTGCTCCACACAGTAGTCCCCANGTGGCCCANTCCC  
GGCCCAGGCTGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGANTGATGA  
ACAGAGTCAGAAGCCCAAAGGAATTGCANTGTGGCAGCATCAGANGTANTNGTCATAAGTGA  
GAGGCGTGTGTTGANTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTcantt  
AAAGGGNCCAAGNTAAATTTGTATTGGTTCATGTAGTGAAGTCAAANTGTTATTcagagatg  
TTTAATGCATATTTAANTTATTTAATGTATTTcATNTCATGTTTTCTTATTGTCACAAGGGT  
ACAGTTAATGCTGCGTGCTGCTGAANTCTGTTGGGTGAANTGGTATTGCTG

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**FIGURE 116**

GGCCCTTGGGGAGCTGGAGCCCAGCATGCTGGGGAGTGCGGTCAGCTCCACACAGTAGTCCC  
CACGTGGCCCACTCCCGGCCAGGCTGCTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGC  
TCCTTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACG  
TACTCGTCATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGC  
AGTGCTTTGTTCACTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAA  
CTGTTATTCAGAGATGTTTAATGCATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTT  
TTATTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTAT  
TGCTGCTGGAGGGCTGTGGGCTCCTCTGTCTCTGGAGAGTCTGGTCATGTGGAGGTGGG

**FIGURE 117**

GCGAGCTCCGGGTGCTGTGGCCCGGCCTTGGCGGGGCGGCCTCCGGCTCAGGCTGGCTGAGA  
GGCTCCCAGCTGCAGCGTCCCCGCCCCGCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCC  
CTCGGGGACCAAACAAGCCTGGCAGGGTCTCACTTTGTTGCCAGGCTGGAGTTCAGTGCCA  
TGATCATGGTTTACTGCAGCCTTGACCTCCTGGGTTCAGCGATCCTGCTGAGTAGCTGGGA  
CTACAGGACAAAATTAGAAGATCAAAATGGAAAATATGCTGCTTTGGTTGATATTTTTCACC  
CCTGGGTGGACCCTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAA  
GGTACCCCGGATTGTCAGTGAAAGGACTTTCCATCTCACCAGCCCCGCATTTGAGGCAGATG  
CTAAGATGATGGTAAATACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCAACTCCCAGC  
CTTTCTGAATTGGAGGATTATCTTTCCCTATGAGACTGTCTTTGAGAATGGCACCCGAACCTT  
AACCAGGGTGAAAGTTCAAGATTTGGTTCTTGAGCCGACTCAAAATATCACCACAAAGGGAG  
TATCTGTTAGGAGAAAGAGACAGGTGTATGGCACCGACAGCAGGTTTACGATCTTGGACAAA  
AGGTTCTTAACCAATTTCCCTTTTCAGCACAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCAT  
TCTCATTTCCCCTCAGCATGTTCTAACTGCTGCCCACTGTGTTTCATGATGGAAAGGACTATG  
TCAAAGGGAGTAAAAAGCTAAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAG  
AAACGTCGAGGTTCTAAGAGGAGCAGGAGAGAAGCTAGTGGTGGTGACCAAAGAGAGGGTAC  
CAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAAGAAGAAAAAATCTGGCCGGGGTC  
AGAGGATTGCCGAAGGGAGGCCTTCCTTTCACTGGACCCGGGTCAAGAATAACCCACATTCGG  
AAGGGCTGGGCACGAGGAGGCATGGGGGACGCTACCTTGGACTATGACTATGCTCTTCTGGA  
GCTGAAGCGTGCTCACAAAAGAAATACATGGAACCTGGAATCAGCCCAACGATCAAGAAAA  
TGCTTGGTGAATGATCCACTTCTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTAT  
CGGTTTTGCACTGTGTCCGACGAATCCAATGATCTCCTTTACCAATACTGCGATGCTGAGTC  
GGGCTCCACCGGTTCCGGGGTCTATCTGCGTCTGAAAGATCCAGACAAAAGAATTGGAAGC  
GCAAAATCATTGCGGTCTACTCAGGGCACCAGTGGGTGGATGTCCACGGGGTTCAGAAGGAC  
TACAACGTTGCTGTTTCGCATCACTCCCCTAAAATACGCCCAGATTTGCCTCTGGATTACGG  
GAACGATGCCAATTGTGCTTACGGCTAACAGAGACCTGAAACAGGGCGGTGTATCATCTAAA  
TCACAGAGAAAACCAGCTCTGCTTACCGTAGTGAGATCACTTCATAGGTTATGCCTGGACTT  
GAACTCTGTCAATAGCATTTCACATTTTTTCAAATCAGGAGATTTTCGTCCATTTAAAAAA  
TGTATAGGTGCAGATATTGAACTAGGTGGGCACTTCAATGCCAAGTATATACTCTTCTTTA  
CATGGTGATGAGTTTCATTTGTAGAAAAATTTTGTGCTTCTTAAAAATTAGACACACTTT  
AAACCTTCAAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTCTCAGGGTCC  
TACTCTAAGAAGAATCTAATAGGATGCTGGTTGTGTATTAAATGTGAAATTGCATAGATAAA  
GGTAGATGGTAAAGCAATTAGTATCAGAATAGAGACAGAAAGTTACAACACAGTTTGTACTA  
CTCTGAGATGGATCCATTCAGCTCATGCCCTCAATGTTTATATTGTGTTATCTGTTGGGTCT  
GGGACATTTAGTTTAGTTTTTTTTGAAGAATTACAAATCAGAAGAAAAAGCAAGCATTATAAA  
CAAACTAATAACTGTTTTACTGCTTTAAGAAATAACAATTACAATGTGTATTATTTAAAAA  
TGGGAGAAATAGTTTGTCTATGAAATAAACCTAGTTTAGAAATAGGGAAGCTGAGACATTT  
TAAGATCTCAAGTTTTTATTTAACTAATACTCAAAATATGGACTTTTCATGTATGCATAGGG  
AAGACACTTCACAAATTATGAATGATCATGTGTTGAAAGCCACATTATTTTATGCTATACAT  
TCTATGTATGAGGTGCTACATTTTATAGGACAAAGAATTCTGTAATCTTTTTCAAGAAAGAGT  
CTTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGGTGAATTCTCTGATTAG  
TAATTTTAGATATGTCCTTTCCTAAAAATGAATAAAATTTATGAATATGA

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**FIGURE 118**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253

<subunit 1 of 1, 413 aa, 1 stop

<MW: 47070, pI: 9.92, NX(S/T): 3

MENMLLWLIFFTPGWTLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFAEADAKMMVNTVC  
GIECQKELPTPSLSELEDYLSYETVFENGTRTLTRVKVQDLVLEPTQNIITTKGVSVRRKRQV  
YGTDSRFSILDKRFLTNFPFSTAVKLSTGCSGILISPQHVLTAHCVHDGKDYVKGSKKLRV  
GLLKMRNKSGGKKRRGSKRSRREASGGDQREGTREHLQERAKGRRRKKSGRGQRIAEGRPS  
FQWTRVKNTHIPKGWARGGMDATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS  
GFDNDRADQLVYRFCSVSDENLLYQYCDAESGSTGSGVYLRLKDPDKKNWKRKIIAVYSG  
HQWVDVHGVQKDYNVAVRITPLKYAQICLWIHGNDANCAYG

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 90-93; 110-113 and 193-196

Glycosaminoglycan attachment site.

amino acids 236-239

Serine proteases, trypsin family, histidine active site.

amino acids 165-170

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**FIGURE 119**

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCAGTACTGGAT  
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTCAGTGTCCGATTCTGATTCCGGCAAGG  
ATCCAAGCATGGGAATGCTGCCGTCGGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTC  
CTGCTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTG  
GGGCCCATGGAGTGAATGCTCACGCACCTGCGGGGGAGGGGCCTCCTACTCTCTGAGGCGCT  
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC  
TGCCCACCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA  
CCATGGCCAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCA  
AGTGCCAAGCCAAAGGAACAACCCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACG  
CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGA  
TCACCAGCTGGGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCA  
CCTGCCGGCTGGTCCGAGGGCAGTATAAATCCCAGCTCTCCGCAACCAAATCGGATGATACT  
GTGGTTGCACTTCCCTATGGAAGTAGACATATTCGCCTTGTCTTAAAAGGTCCTGATCACTT  
ATATCTGGAAACCAAACCCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAA  
CTTTCCTTGTGGACAATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGA  
ATGGCTGGACCACTCACAGCAGATTTCAATTGTCAAGATTCGTAACCTCGGGCTCCGCTGACAG  
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTC  
CTTGCTCAGCAACCTGTGGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG  
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC  
CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGC  
CTTATGACCTCTACCATCCCCCTTCCTCGGTGGGAGGGCCACCCCATGGACCGCGTGCTCCTCC  
TCGTGTGGGGGGGGCATCCAGAGCCGGGCAGTTTCCTGTGTGGAGGAGGACATCCAGGGGCA  
TGTCACCTTCAGTGGAAGAGTGGAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCT  
GCAACATTTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT  
GGCCAGGGCCTCAGATACCGTGTGGTCCTCTGCATCGACCATCGAGGAATGCACACAGGAGG  
CTGTAGCCCCAAAACAAAGCCCCACATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATA  
AACCCAAAGAGAACTTCCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA  
GAAGAAGGAGCTGCTGTGTCAGAGGAGCCCTCGTAAGTTGTAAAAGCACAGACTGTTCTATA  
TTTGAACTGTTTTGTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTCATGGGTTCTGA  
ACTAAGTGTAATCATCTCACCAAGCTTTTTGGCTCTCAAATTAAAGATTGATTAGTTTCAA  
AAAAAAAAA

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**FIGURE 120**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847

<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

MECCRRATPGTLLLFLAFLLLSSRTARSEEDRDGLWDAWGPWSECSRTC GGGASYS LRRLS  
SKSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNDPDNPSLKCQ  
AKGTTLVVELAPKVLDTGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR  
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLVKGPDLHLYLETKTLQGTKGENSLSSSTGTFL  
VDNSSVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFPCS  
ATCGGGYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYD  
LYHPLPRWEATPWTACSSSCGGGIQSRAVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI  
FDCPKWLAQEWSPCTVTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK  
EKL PVEAKLPWFKQAQAELEEGA AVSEEPS

Important features:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 251-254

Thrombospondin 1

amino acids 385-399

von Willebrand factor type C domain proteins

amino acids 385-399, 445-459 and 42-56

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**FIGURE 121**

CGGACGCGTGGGCGGCGGCTGCGGAACTCCCGTGGAGGGGCCGGTGGGCCCTCGGGCCTGAC  
AGATGGCAGTGGCCACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCG  
GCCCCCGGTTCGTGGGGCCCAGGGTCCAGCGGCTGCGCAGAGGCGGGGACCCCGGCCTCAT  
GCACGGGAAGACTGTGCTGATCACCGGGGCGAACAGCGGCCTGGGCGCGCCACGGCCGCCG  
AGCTACTGCGCCTGGGAGCGCGGGTGATCATGGGCTGCCGGGACCGCGCGCGCGCCGAGGAG  
GCGGCGGGTCAGCTCCGCCGCGAGCTCCGCCAGGCCGCGGAGTGCGGCCAGAGCCTGGCGT  
CAGCGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCG  
CCTTCTGCCAGGAAATGCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGCAGGG  
ATCTTCCAGTGCCCTTACATGAAGACTGAAGATGGGTTTGAGATGCAGTTCGGAGTGAACCA  
TCTGGGGCACTTTCTACTACCAATCTTCTCCTTGGACTCCTCAAAGTTCAGCTCCCAGCA  
GGATTGTGGTAGTTTCTTCCAACTTTATAAATACGGAGACATCAATTTTGATGACTTGAAC  
AGTGAACAAAGCTATAATAAAAGCTTTTGTATAGCCGGAGCAAAGTGGCTAACATTCTTTT  
TACCAGGGAAGTAGCCCGCCGCTTAGAAGGCACAAATGTCACCGTCAATGTGTTGCATCCTG  
GTATTGTACGGACAAATCTGGGGAGGCACATACATTCCACTGTTGGTCAAACCACTCTTC  
AATTTGGTGTGATGGGCTTTTTTCAAAGTCCAGTAGAAGGTGCCAGACTTCCATTTATTT  
GGCCTCTTCACCTGAGGTAGAAGGAGTGTCAGGAAGATACTTTGGGGATTGTAAAGAGGAAG  
AACTGTTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAAGTCTGGGATATCAGTGAAGTG  
ATGGTTGGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTTTATAAAAGTGCATATCAG  
TTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTACTTGAAGAAAAGAATTTTG  
ATATTGGAATAGCCTGCTAAGAGGTACATGTGGGTATTTTGGAGTTACTGAAAATTATTTT  
TGGGATAAGAGAATTTTCAAGCAAGATGTTTTAAATATATATAGTAAGTATAATGAATAATA  
GTACAATGAAAATAACAATTATATTGTAAATTATAACTGGGCAAGCATGGATGACATATTA  
ATATTTGTCAGAATTAAGTGAAGTCAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGTT  
TCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTGTTGTGTGGAAATTATCTGC  
CTGGTGTGTGCACACAAGTCTTACTTGAATAAATTTACTGGTAC

**FIGURE 122**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747

<subunit 1 of 1, 336 aa, 1 stop

<MW: 36865, pI: 9.15, NX(S/T): 2

MAVATAAAVLAAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAE  
LLRLGARVIMGCRDRARAEAAAGQLRRELROAAECGPEPGVSGVGELIVRELDLASLRSVRA  
FCQEMLQEEPRLDVLINNAGIFQCPYMKTEDGFEMQFGVNHLLGHFLLTNLLLGLLKSSAPSR  
IVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSKLANILFTRELARRLEGTVNVTNVNLHPG  
IVRTNLGRHIHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSGRYFGDCKEEE  
LLPKAMDESVARKLWDISEVMVGLLK

Important features:

Signal peptide:

amino acids 1-21

Short-chain alcohol dehydrogenase family protein

amino acids 134-144, 44-56 and 239-248

N-glycosylation site.

amino acids 212-215 and 239-242

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**FIGURE 123**

GGGGATTGTAAAGAGGAAGNACTGTGCCCAAAGNTATGGATGAATCTGTTGCAAGAAAATTN  
TGGGATATCAGTGAAGTGATGGTTNGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTT  
TATAAACTGCATATCAGTTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACT  
TGAAGAAAAGAATTTTGATATTGGAATAGCCTGNTAAGAGGNACATGTGGGTATTTTGGAG  
TTACTGAAAAATTATTTTGGGATAAGAGAATTCAGCAAAGATGTTTTAAATATATATAGT  
AAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATTGTAAAATTATACTGGGCA  
AGCATGGATGACATATTAATATTTGTCAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTT  
TTCAAGTATCTTTGAGTTTCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTT  
TGTGTGGAAATTATCTGCCTGGCTT

**FIGURE 124**

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCCGCTCCCGGAGCCCAGCC  
CTTTCCTAACCCAACCCAACCTAGCCCAGTCCCAGCCGCCAGCGCCTGTCCCTGTCACGGAC  
CCCAGCGTTACCAATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCT  
GCTCCTGGTAACTTGGGTTTTTACTCCTGTAACAACTGAAATAACAAGTCTTGCTACAGAGA  
ATATAGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTTATGCTGACTGGTGT  
CGTTTCAGTCAGATGTTGCATCCAATTTTTGAGGAAGCTTCCGATGTCATTAAGGAAGAATT  
TCCAAATGAAAATCAAGTAGTGTGTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCC  
AGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATGGGATGATGATGAAG  
AGAGAATACAGGGGTGAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAAG  
TGACCCCATTCAGAAATTCGGGACTTAGCAGAAATCACCCTCTTGATCGCAGCAAAAGAA  
ATATCATTGGATATTTTGAGCAAAAGGACTCGGACAACCTATAGAGTTTTTGAACGAGTAGCG  
AATATTTTGCATGATGACTGTGCCTTTCTTTCTGCATTTGGGGATGTTTCAAACCGGAAAG  
ATATAGTGGCGACAACATAATCTACAAACCACCAGGGCATTCTGCTCCGGATATGGTGTACT  
TGGGAGCTATGACAAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTTCCTCTT  
GTCCGAGAAATAACATTTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCAT  
ACTCTTTCACATGAAAGAAGATACAGAAAGTTTAGAAATATTCAGAAATGAAGTAGCTCGGC  
AATTAATAAGTGAAAAAGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACAT  
CCTCTTCTGCACATACAGAAACTCCAGCAGATTGTCCTGTAATCGCTATTGACAGCTTTAG  
GCATATGTATGTGTTTGGGAGACTTCAAAGATGTATTAATTCCTGGAAACTCAAGCAATTCTG  
TATTTGACTTACATTCTGGAAACTGCACAGAGAATTCCATCATGGACCTGACCCAACTGAT  
ACAGCCCCAGGAGAGCAAGCCCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAA  
ACTAGCACCCAGTGAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTTTAAAAAACTTG  
AAAAACAGTTTGTAAGCCTTTCAACAGCAGCATCAACCTACGTGGTGGAAATAGTAAACCTA  
TATTTTCATAATTCTATGTGTATTTTTATTTTGAATAAACAGAAAGAAATTTAAAAA  
AAAAA



**FIGURE 125**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57689

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46927, pI: 5.21, NX(S/T): 0

MHPAVFLSLPDLRCSLLLLVTWVFTPVTTEITSLATENIDEILNNADVALVNFYADWCRFSQ  
MLHPIFEEASDVIKEEFPNENQVVFARVDCDQHS DIAQRYRISKYPTLKLFRNGMMMKREYR  
GQRSVKALADYIRQOKSDPIQEIRD LAEITTLDRSKRNIIGYFEQKSDNYRVFERVANILH  
DDCAFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNW IQDKCVPLVREI  
TFENGEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH  
IQKTPADCPVIAIDSFRHMYVFGDFKDV LIPGKLKQFVFDLHSGKLHREFHHGPDPTDTAPG  
EQAQDVASSPPESSFQKLAPSEYRYTLLRDRDEL

Important features:

Signal peptide:

amino acids 1-29

Endoplasmic reticulum targeting sequence.

amino acids 403-406

Tyrosine kinase phosphorylation site.

amino acids 203-211

Thioredoxin family proteins

amino acids 50-66

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## FIGURE 126

ATTAAGGAAGAATTTCCAAATGAAAATCAAGTAGTNTTTGCCAGAGTNGATTGTGATCAGCA  
CTCTGACATAGCCCAGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATG  
GGATGATGATGAAGAGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTA

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**FIGURE 127**

AGAGGCCTCTCTGGAAGTTGTCCCGGGTGTTCGCCGCNNGAGCCCGGGTCGAGAGGACNAGG  
TGCCGCTGCCTGGAGAATCCTCCGCTGCCGTGCGCTCCCGGAGCCCAGCCCTTTCCTAACCC  
AACCCAACCTAGCCCNGTCCCAGCCGCCAGCGCCTGTCCCTGTCNCGGANCCCAGCGTNACC  
ATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCTCCTGGTAAC  
TTGGGTTTTTACTCCTGTAACAACCTGAAATAACNNGTCTTGATACNNAGAATATAGATGAAA  
TTTTAAACNATGCTGATGTGGCTTTAGTCAATTTTTATGCTGACTGGTGTCTGTTTCAGTCAG  
ATGTGGCATCCAATTTTTGAGGANGCTTCCGATGTCATTAAGGAAGAATTTCCAAATGAAAA  
TCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATACAGGA  
TAAGCAAATACCCAACCCTCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATACAGG  
GGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGC

**FIGURE 128**

GCCCACGCGTCCGATGGCGTTCACGTTGCGGGCCTTCTGCTACATGCTGGCGCTGCTGCTCA  
CTGCCGCGCTCATCTTCTTCGCCATTTGGCACATTATAGCATTTGATGAGCTGAAGACTGAT  
TACAAGAATCCTATAGACCAGTGTAATACCCTGAATCCCCCTGTACTCCCAGAGTACCTCAT  
CCACGCTTTCTTCTGTGTCATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATA  
TGCCCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGA  
CTCTATGACCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCAGAAGGAAGGATG  
GTGCAAATTAGCTTTTTTATCTTCTAGCATTTTTTTTACTACCTATATGGCATGATCTATGTTT  
TGGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCAC  
CAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT  
TACTTTAAAAAATGACTCCTTATTTTTTTAAATGTTTCCACATTTTTTGCTTGTGGAAAGACTG  
TTTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAAT  
GATTACCTCTGGTGTGACAGGTTTGAACCTGCACTTCTTAAGGAACAGCCATAATCCTCTG  
AATGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGTGTTATAGGAACTTGTA  
GGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGC  
TTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAACTTCATGGGTTTCCTCATCTGTC  
ATGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTTCCCTTCGCTT  
GAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAA  
TATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAATATATGCTGAATTACTT  
GTGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTTTATTTGTAAGACATTACTTATTAAG  
AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGG  
TACTACAGATTTTCAAAACTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTCCCTTTAGT  
GCAATACAATAAAACTCTGAAATTAAGACTC

**FIGURE 129**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330

<subunit 1 of 1, 144 aa, 1 stop

<MW: 16699, pI: 5.60, NX(S/T): 0

MAFTFAAFCYMLALLLTAAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFF  
CVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLA  
FYLLAFFYYLYGMIYVLVSS

Important features:

Signal peptide:

amino acids 1-20

Type II transmembrane domain:

amino acids 11-31

Other transmembrane domain:

amino acids 57-77 and 123-143

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**FIGURE 130**

ATTATAGCATTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAATACCCTG  
AATCCCCTTGTA TACTCCCAGAGTACCTCATCCACGCTTCTTCTGTGTCATGTTTCTTTGTGC  
AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCCTCTTGGCATATCATATTTGGAGGTATA  
TGAGTAGACCAGTGATGAGTGGCCCAGGACTCTATGACCCTACAACCATCATGAATGCAGAT  
ATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTTTTTATCTTCTAGCATTTTT  
TTACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAACACACACAGAAGAATT  
GGTCCAGTTAAGTGCATGCAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGT  
CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAATG

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**FIGURE 131**

CGGACGCGTGGGGGAAACCCTTCCGAGAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGG  
GAACAAGATGGCGGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACCTGGGGCTCCCGCCGC  
TGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTCTGGGGACCGCTTCGGCTGAAGCATTGAC  
TCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGACAC  
CTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTC  
AGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACA  
GAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCC  
ATTTCGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTC  
CTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACC  
TCTTCATGGACTTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCCAGTCTAAGCC  
AGAAATCCAGTACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAA  
GCAAAATGTCCTATCTGCAAATGAGAAATTCACAAGCGCACAGGAATTTTCTTGAAGATGGA  
GAAAGTGATGGCTTTTTTAAGATGCCTCTCTCTTAACTCTGGGTGGATTTTAACTACAACTCT  
TGTCTCTCGGTGATGGTATTGCTTTGGATTTGTTGTGCAACTGTTGCTACAGCTGTGGAGC  
AGTATGTTCCCTCTGAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAG  
CTAAACAGATATCCAGCTTCTTCTCTTGTGGTTGTTAGATCTAAACTGAAGATCATGAAGA  
AGCAGGGCCTCTACCTACAAAAGTGAATCTTGCTCATTCTGAAATTTAAGCATTTTTCTTTT  
AAAAGACAAGTGTAATAGACATCTAAAATTCCACTCCTCATAGAGCTTTTAAAATGGTTTCA  
TTGGATATAGGCCTTAAGAAATCACTATAAAATGCAATAAAGTTACTCAAATCTGTG



**FIGURE 132**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26847

<subunit 1 of 1, 323 aa, 1 stop

<MW: 36223, pI: 5.06, NX(S/T): 1

MAAPKGS LWVRTQLGLPPLLLLT MALAGGSGTASAEAFDSVLGDTASCHRA CQLTYPLHTYP  
KEEELYACQ RGCRLFSICQFVDDGIDLNR TKLECESACTEAYSQSDEQYACHLGCQNQLPFA  
ELRQEQLMSLMPKMHL LFP LTLVRSFWSDMMDSAQS FITSSWTFY LQADDGKIVIFQSKPEI  
QYAPHLEQEPTNLRESSLSKMSYLQMRNSQAHRNFLEDGESDGFLRCLSLNSGWILTTTLVL  
SVMVLLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVR SKTEDHEEAG  
PLPTKVNLAHSEI

Important features:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 241-260

N-glycosylation site.

amino acids 90-93

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**FIGURE 133**

TTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGCACACCTACCC  
TAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTTG  
TGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA  
TATTCCTCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTGCGC  
TGAAGTGAAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTCCTCTAA  
CTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGC

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**FIGURE 134**

CACACTGGCCGGATCTTTTAGAGTCCTTTGACCTTGACCAAGGGTCNGGAAAACAGCAACAA  
GCTGAGCTGCTGTGACAGAGGGAACAAGATGGCGGCGCCGAAGGGAGCCTTTGGGTGAGGAC  
CCAAC TGGGGCTCCCGCCGCTGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTTCGGGGACCG  
CTTCGGCTGAAGCATTGACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAG  
TTGACCTACCCCTTGACACACCTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTG  
CAGGCTGTTTTCAATTTGTCAGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGG  
AATGTGAATCTGCATGTACAGAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTT  
GGTTGCCAGAATCAGCTGCCATTCGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCC  
AAAAATGCACCTACTCTTTCCTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACT  
CCGC

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**FIGURE 135**

GCGAGGTGGCGATCGCTGAGAGGCAGGAGGGCCGAGGCGGGCCTGGGAGGCGGCCCCGGAGGT  
GGGGCGCCGCTGGGGCCGGCCCGCACGGGCTTCATCTGAGGGCGCACGGCCCGCGACCGAGC  
GTGCGGACTGGCCTCCCAAGCGTGGGGCGACAAGCTGCCGGAGCTGCAATGGGCGCGGCTG  
GGGATTCTTGTGTTGGCCTCCTGGGCGCCGTGTGGCTGCTCAGCTCGGGCCACGGAGAGGAGC  
AGCCCCCGGAGACAGCGGCACAGAGGTGCTTCTGCCAGGTTAGTGGTACTTGGATGATTGT  
ACCTGTGATGTTGAAACCATTTGATAGATTTAATAACTACAGGCTTTTCCCAAGACTACAAAA  
ACTTCTTGAAAGTGACTACTTTAGGTATTACAAGGTAAACCTGAAGAGGCCGTGTCCTTTCT  
GGAATGACATCAGCCAGTGTGGAAGAAGGGACTGTGCTGTCAAACCATGTCAATCTGATGAA  
GTTCTTGATGGAATTAAATCTGCGAGCTACAAGTATTCTGAAGAAGCCAATAATCTCATTGA  
AGAATGTGAACAAGCTGAACGACTTGGAGCAGTGGATGAATCTCTGAGTGAGGAAACACAGA  
AGGCTGTTCTTCAGTGGACCAAGCATGATGATTCTTCAGATAACTTCTGTGAAGCTGATGAC  
ATTCAGTCCCCCTGAAGCTGAATATGTAGATTTGCTTCTTAATCCTGAGCGCTACACTGGTTA  
CAAGGGACCAGATGCTTGGAAAATATGGAATGTCATCTACGAAGAAAACCTGTTTTAAGCCAC  
AGACAATTAAAAGACCTTTAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGAACACT  
TTTTACAGTTGGCTAGAAGTCTCTGTGTAGAAAAAAGAGCATTCTACAGACTTATATCTGG  
CCTACATGCAAGCATTAAATGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAG  
AAAAGAAATGGGGACACAACATTACAGAATTTCAACAGCGATTTGATGGAATTTTGACTGAA  
GGAGAAGGTCCAAGAAGGCTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTT  
ATCCAAAGTGTTACCATTTCTTCGAGCGCCAGATTTTCAACTCTTTACTGGAAATAAAATTC  
AGGATGAGGAAAACAAAATGTTACTTCTGGAAATACTTCATGAAATCAAGTCATTTCTTTG  
CATTTTGATGAGAATTCATTTTTTGCTGGGGATAAAAAAGAAGCACACAACTAAAGGAGGA  
CTTTGACTGCATTTTAGAAATATTTCAAGAATTATGGATTGTGTTGGTTGTTTTAAATGTC  
GTCTGTGGGGAAAGCTTCAGACTCAGGGTTTGGGCACTGCTCTGAAGATCTTATTTTCTGAG  
AAATTGATAGCAAATATGCCAGAAAGTGGACCTAGTTATGAATTCCATCTAACCAGACAAGA  
AATAGTATCATTATTCAACGCATTTGGAAGAATTTCTACAAGTGTGAAAGAATTAGAAAAC  
TCAGGAACTTGTTACAGAATATTCATTAAGAAAACAAGCTGATATGTGCCTGTTTCTGGAC  
AATGGAGGCGAAAGAGTGGAATTTCAATCAAAGGCATAATAGCAATGACAGTCTTAAGCCAA  
ACATTTTATATAAAGTTGCTTTTGTAAAGGAGAATTATATTGTTTTAAGTAAACACATTTTT  
AAAAATTGTGTTAAGTCTATGTATAATACTACTGTGAGTAAAAGTAATACTTTAATAATGTG  
GTACAAATTTTAAAGTTTAATATTGAATAAAAGGAGGATTATCAAATTAATAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 136**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53974  
<subunit 1 of 1, 468 aa, 1 stop  
<MW: 54393, pI: 5.63, NX(S/T): 2  
MGRGWGFLFGLLGAVWLLSSGHGEEQPPETAARCFQVSGYLDDCTCDVETIDRFNNYRLF  
PRLQKLLESDFRYKVNLRPCPFWNDISQCGRRDCAVKPCQSDEVPDGIKSASYKYSEEA  
NNLIEECEQAERLGAVDESLSEETQKAVLQWTKHDDSSDNFCEADDIQSPEAEYVDLLLNP  
RYTGKGPDAWKIWNVIYEENCFKPQTIKRPLNPLASGQGTSEENTFYSWLEGLCVEKRAF  
RLISGLHASINVHLSARYLLQETWLEKKWGHNITEFQQRFDGILTEGEGPRRLKNLYFLYLI  
ELRALSQVLPFFERPDLFTGNKIQDEENKMLLLEILHEIKSFPLHFDENSFFAGDKKEAH  
KLKEDFRLHFRNISRIMDCVGCFCRLWGKLQTQGLGTALKILFSEKLIANMPESGPSYEFH  
LTRQEIVSLFNAFGRISTSVKELENFRNLLQNIH

**Important features:****Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 280-283 and 384-387

**Amidation site.**

amino acids 94-97

**Glycosaminoglycan attachment site.**

amino acids 20-23 and 223-226

**Aminotransferases class-V pyridoxal-phosphate**

amino acids 216-222

**Interleukin-7 proteins**

amino acids 338-343

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FIGURE 137

GCTGGAAATATGGATGTCATCTACGAGAACTGTTTTAAGCCACAGACAATTAAAAGACCTT  
TAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGNACACTTTTTACAGTTGGCTAGAA  
GGTCTCTGTGTAGAAAAAAGAGCATTCTACAGACTTATATCTGGCCTACATGCAAGCATTAA  
TGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAGAAAAGAAATGGGGACACA  
ACATTACAGAATTTNAACAGCGATTTGATGGAATTTTGACTGAAGGAGAAGGTCCAAGAAGG  
CTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTTATCCAAAGTGTTACCATT  
CTTNGAGCGCCCAGATTTTCAACTNTTTACTGGAAATAAAATTTCAGGATGAGGNAAACAAA  
TGTTACTTTTGGAAATACTTCATGAAATCAAGTCATTCCTTTGCATTTTGATGAGAATTCA  
TTTTTTTGCTG

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**FIGURE 138**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTGGGAGGGGGCAGGATGGGAGGGAA  
AGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAAC  
CGATCAGGCATGGAACTCCCCTTCGTCACTCACCTGTTCTTGCCCCCTGGTGTTCTTGACAGG  
TCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCTATTCCCAGGGCCACCAGAAG  
CTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGATGCTGGTGGGC  
GCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGGACGTTTATCGCTGCCCTGTAGGGGG  
GGCCCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTCATCTC  
ATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTAGAGACAGATGGTGATGGGGGATTC  
ATGGTGAGCTAAGGAGAGGGTGGTGGCAGTGTCTCTGAAGGTCCATAAAAGAAAAAGAGAA  
GTGTGGTAAGGGAAAATGGTCTGTGTGGAGGGGTCAAGGAGTTAAAAACCCTAGAAAGCAAA  
AGGTAGGTAATGTCAGGGAGTAGTCTTCATGCCTCCTTCAACTGGGAGCATGTTCTGAGGGT  
GCCCTCCCAAGCCTGGGAGTAACTATTTCCCCCATCCCCAGGCCTGTGCCCTCTCTGGTCT  
CGTGCTTGTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCCCGTGTGGATGCTTCATTCCA  
GCCTCAGGGAAGCCTGGCACCCACTGCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGGTT  
CCCAGAAGGAGATACTGGGTGGGAAAAAGATGGGGCAAAGCGGTATGATGCCTGGCAAAGGG  
CCTGCATGGCTATCCTCATTGCTACCTAATGTGCTTGCAAAAGCTCCATGTTTCCTAACAGA  
TTCAGACTCCTGGCCAGGTGTGGTGGCCACACCTGTAATTCTAGCACTTTGGGAGGCCAAG  
GTGGGCAGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAACTCCAT  
CTCTACTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA  
ATCTACTCGGGAGGCTAAGACAGGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTG  
AGCCAAGATTGTGCCTCTGCACTCTAGCGTGGGTGACAGAGTAAGCGAGACTCCATCTCAAA  
AATAATAATAATAATAATTTCAGACTCCTTATCAGGAGTCCATGATCTGGCCTGGCACAGTAA  
CTCATGCCTGTAATCCCAACATTTTGGGAGGCCAACGCAGGAGGATTGCTTGAGGTCTGGAG  
GTTTGAGACCAGCCTGGGCAACATAGAAAGACCCCATCTCTAAATAAATGTTTTAAAAAT



**FIGURE 139**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039  
><subunit 1 of 1, 124 aa, 1 stop  
><MW: 13352, pI: 5.99, NX(S/T): 1  
MELPFVTHLFLPLVFLTGLCSPFNLDEHHPRLFPGPPEAEFGYSVLQHVGGGQRWMLVGAPW  
DGPSGDRRGDVYRCPVGGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETGDGGFMVS

Important features:

Signal peptide:

amino acids 1-22

Cell attachment sequence.

amino acids 70-73

N-glycosylation site.

amino acids 98-101

Integrins alpha chain proteins

amino acids 67-81

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**FIGURE 140**

CACAGTTCCCCACCATCACTCNTCCCATTCCTTCCAACCTTTATTTTATAGCTTGCCATTGGGA  
GGGGGCAGGATGGGAGGGGAAAGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGAC  
TTCTCATACTGGACAGAAACCGATCAGGCATGGAACCTCCCCTTCGTCACTCACCTGTTCTTG  
CCCCTGGTGTTCCCTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCT  
ATTCCCAGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGAC  
AGCGATGGATGCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTT  
TATCGCTGCCCTGTAGGGGGGGCCCCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTA  
CCAACCTGGGAAATTCATCTCATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTAGAGA  
CAGATGGTGATGG

**FIGURE 141**

AAAGTTACATTTTCTCTGGAACCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG  
GGCAGAAAGGAGGGTGCTTCGGAGCCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACA  
ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT  
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA  
AATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT  
ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCCCTCAGAACCTC  
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTGATCGCGCCTGGAGA  
AACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT  
GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTGATGTCACTGATGACATC  
ACGGCCACTGTGCCATAACAACCTTCGTGTCAGGGCCACATTGGGCTCACAGACCTCAGCCTG  
GAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA  
TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC  
CTTGTTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAAATGGTGAGGAGTGG  
GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA  
CATTCGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA  
GGAGAGGCCATTCCCCTGGTACTGGCCCTGTTTGCCTTTGTTGGCTTCATGCTGATCCTTGT  
GGTCGTGCCACTGTTTCGTCTGGAAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGG  
TGGTCCTCCCAGACACCTTGAAAATAACCAATTCACCCCAGAAGTTAATCAGCTGCAGAAGG  
GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCAGGGCCTGGAT  
CTCATAGGTTTGCGGAAGGGCCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC  
ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA  
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC  
TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC  
CTGGGAAAAGTGACTTCATCCCTTCGGTCCTAAGTTTTCTCATCTGTAATGGGGGAATTACC  
TACACACCTGCTAAACACACACACACAGAGTCTCTCTCTATATATACACACGTACACATAAA  
TACACCCAGCACTTGCAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTCAG  
TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT  
GGCTTGGAGAGCCCCTTTCCCAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG  
TGTTGAGTTCACCTCAAGCCCAATGCCGGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT  
AGGTGACCTGGAGGAAGGTCACAGCCCACTGAAAATGGGATGTGCATGAACACGGAGGATC  
CATGAACACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT  
GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC  
TGTTGGTAAAGTACAGAATTCAGCAAATAAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA  
AAAAAAA

**FIGURE 142**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57033

<subunit 1 of 1, 311 aa, 1 stop

<MW: 35076, pI: 5.04, NX(S/T): 2

MQTFTMVLEEIWTSLEFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIAPGE  
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTS  
SILKHPFNRNSTILTRPGMEITKDGFHLVIELEDLGPQFEFLVAYWRREPGAEHVKMVRSG  
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPVLALFAFVGFMILILV  
VVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation site.

amino acids 40-43 and 134-137

Tissue factor proteins.

amino acids 92-119

Integrins alpha chain proteins

amino acids 232-262

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**FIGURE 143**

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT  
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA  
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG  
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT  
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC  
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA  
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTCTGAATACCAGGGGGAGTACGAGAGCCT  
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG  
ATGTCACTGATGACATCACGGCCACTGTGCCATAACAACCTTTGTGTCAGGGCCACATTGGGC  
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTAC  
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG  
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG  
GTTNGCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCC  
ACATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

**FIGURE 144**

CCCACGCGTCCGCCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGA  
GGCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGA  
GGAGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAG  
GAGGAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAAC  
GGAGAGGAGGTGTGGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGA  
GTAGGAAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAGAGG  
AAAGACACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTG  
GCTGCTTTGGCATTGTTGGGGAAGTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCCT  
GGAGGGACAGGGTCCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGGCAGGGCGTTGGG  
CAGGGGTCCCTCGGAGGCCTCCTGGGGATGGGGGCTGCAGCTCGTCTGAGCGCCCCCTCGAGC  
GCTGGTACTCTGGGCTGCACTGGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGG  
ACTGGTGGAGCTACAAGGATAATCTCCAGGGAACTTCGTGCCAGGGCCTCCTTTCTGGGGC  
CTGGTGAATGCAGCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGA  
GCTGAAGAGGGTTCTTTATGACCCCTTTCTGCCCCATTAAGGCTCAGCACTGGAGGAGAGA  
AGCTCCGGGGGAACCTTGTACAACACCGGCCGACATGTCTCCTTCCTGCCTGCACCCCGACCT  
GTGGTCAATGTGTCTGGAGGTCCCCCTCCTTTACAGCCACCGACTCAGTGAAGTGGGCTGCT  
GTTTGGAGCTCGCGACGGAGCCGGCTCGGAACATCAGATCAACCACCAGGGCTTCTCTGCTG  
AGGTGCAGCTCATTCACTTCAACCAGGAACTCTACGGGAATTTAGCGCTGCCTCCCGCGGC  
CCCAATGGCCTGGCCATTCTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCCATTCTC  
CAGTCGCCTCCTTAACCGCGACACCATCACTCGCATCTCCTACAAGAATGATGCCTACTTTC  
TTCAAGACCTGAGCCTGGAGCTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGC  
TCTCTCAGCACCCCGCCCTGCTCCGAGACTGTCACCTGGATCCTCATTGACCGGGCCCTCAA  
TATCACCTCCCTTCAGATGCACTCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCT  
TCCAGAGCCTCAGCGGTAACAGCCGGCCCCCTGCAGCCCTTGGCCCACAGGGCACTGAGGGGC  
AACAGGGACCCCGGCACCCCGAGAGGGCGCTGCCGAGGCCCCAACTACCGCCTGCATGTGGA  
TGGTGTCCCCCATGGTCGCTGAGACTCCCTTCGAGGATTGCACCCGCCCCGTCTAAGCCTC  
CCCACAAGGCGAGGGGAGTTACCCCTAAAACAAAGCTATTAAAGGGACAGAATACTTA

**FIGURE 145**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34353

<subunit 1 of 1, 328 aa, 1 stop

<MW: 36238, pI: 9.90, NX(S/T): 3

MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLC  
AVGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPL  
LYSHRLSELRLLEFGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSL  
FVNVASTSNPFSLRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITIQGSLSTPPCSE  
TVTWILIDRALNITSLQMHSRLRLSQNPSPQIFQSLSGNSRPLQPLAHRALRGNRDPRHPER  
RCRGPNYRLHVDGVPHGR

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 177-199

N-glycosylation site.

amino acids 118-121, 170-173 and 260-263

Eukaryotic-type carbonic anhydrases proteins

amino acids 222-270, 128-164 and 45-92

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**FIGURE 146**

GGCGCCTGGTTCTGCGCGTACTGGCTGTACGGAGCAGGAGCAAGAGGTGCGCGCCAGCCTCC  
GCCGCCGAGCCTCGTTTCGTGTCCCCGCCCTCGCTCCTGCAGCTACTGCTCAGAAACGCTGG  
GGCGCCACCCCTGGCAGACTAACGAAGCAGCTCCCTTCCCACCCCAACTGCAGGTCTAATTT  
TGGACGCTTTGCCCTGCCATTTCTTCCAGGTTGAGGGAGCCGCAGAGGCGGAGGCTCGCGTAT  
TCCTGCAGTCAGCACCCACGTCGCCCCCGGACGCTCGGTGCTCAGGCCCTTCGCGAGCGGGG  
CTCTCCGTCTGCGGTCCCTTGTGAAGGCTCTGGGCGGCTGCAGAGGCCGGCCGTCCGGTTTG  
GCTCACCTCTCCCAGGAAACTTCACACTGGAGAGCCAAAAGGAGTGGAAGAGCCTGTCTTGG  
AGATTTTCTGTTGGGAAATCCTGAGGTCATTATTAATGAAGTGTACCGCGCGGGAGTGGCTCA  
GAGTAACCACAGTGCTGTTTCATGGCTAGAGCAATTCAGCCATGGTGGTTCCCAATGCCACT  
TTATTGGAGAACTTTTGGAAAAATACATGGATGAGGATGGTGAGTGGTGGATAGCCAAACA  
ACGAGGGGAAAAGGGCCATCACAGACAATGACATGCAGAGTATTTTGGACCTTCATAATAAAT  
TACGAAGTCAGGTGTATCCAACAGCCTCTAATATGGAGTATATGACATGGGATGTAGAGCTG  
GAAAGATCTGCAGAATCCTGGGCTGAAAGTTGCTTGTGGGAACATGGACCTGCAAGCTTGCT  
TCCATCAATTGGACAGAATTTGGGAGCACACTGGGGAAGATATAGGCCCCCGACGTTTCATG  
TACAATCGTGGTATGATGAAGTGAAAGACTTTAGCTACCCATATGAACATGAATGCAACCCA  
TATTGTCCATTCAGGTGTTCTGGCCCTGTATGTACACATTATACACAGGTCTGTGTGGGCAAC  
TAGTAACAGAATCGGTTGTGCCATTAATTTGTGTACATAACATGAACATCTGGGGGCAGATAT  
GGCCCAAAGCTGTCTACCTGGTGTGCAATTAATCCCCAAAGGGAAACTGGTGGGGCCATGCC  
CCTTACAAACATGGGCGGCCCTGTTCTGCTTGCCACCTAGTTTTTGGAGGGGGCTGTAGAGA  
AAATCTGTGCTACAAAGAAGGGTCAGACAGGTATTATCCCCCTCGAGAAGAGGAAACAAATG  
AAATAGAACGACAGCAGTCACAAGTCCATGACACCCATGTCCGGACAAGATCAGATGATAGT  
AGCAGAAATGAAGTCATAAGCGCACAGCAAATGTCCCAAATTGTTTCTTGTGAAGTAAGATT  
AAGAGATCAGTGCAAAGGAACAACCTGCAATAGGTACGAATGTCCTGCTGGCTGTTTGGATA  
GTAAAGCTAAAGTTATTGGCAGTGTACATTATGAAATGCAATCCAGCATCTGTAGAGCTGCA  
ATTCAATTATGGTATAATAGACAATGATGGTGGCTGGGTAGATATCACTAGACAAGGAAGAAA  
GCATTATTTTCATCAAGTCCAATAGAAATGGTATTCAAACAATTGGCAAATATCAGTCTGCTA  
ATTCCTTCACAGTCTCTAAAGTAACAGTTCAGGCTGTGACTTGTGAAACAACCTGTGGAACAG  
CTCTGTCCATTTTCATAAGCCTGCTTCACATTGCCCAAGAGTATACTGTCCCTCGTAACTGTAT  
GCAAGCAAATCCACATTATGCTCGTGTAAATTGGAACCTCGAGTTTATTCTGATCTGTCCAGTA  
TCTGCAGAGCAGCAGTACATGCTGGAGTGGTTCGAAATCACGGTGGTTATGTTGATGTAATG  
CCTGTGGACAAAAGAAAGACCTACATTGCTTCTTTTTCAGAATGGAATCTTCTCAGAAAGTTT  
ACAGAATCCTCCAGGAGGAAAGGCATTTCAGAGTGTGTTGCTGTGTGTAAGTGAATACTTG  
GAAGAGGACCATAAAGACTATTCCAAATGCAATATTTCTGAATTTTGTATAAACTGTAACA  
TTACTGTACAGAGTACATCAACTATTTTCAGCCCAAAAAGGTGCCAAATGCATATAAATCTT  
GATAAACAAAGTCTATAAAATAAAACATGGGACATTAGCTTTGGGAAAAGTAATGAAAATAT  
AATGGTTTTAGAAATCCTGTGTTAAATATTGCTATATTTTCTTAGCAGTTATTTCTACAGTT  
AATTACATAGTCATGATTGTTCTACGTTTCATATATTATATGGTGCTTTGTATATGCCACTA  
ATAAAATGAATCTAAACATTGAATGTGAATGGCCCTCAGAAAATCATCTAGTGCATTTAAAA  
ATAATCGACTCTAAAACTGAAAGAAACCTTATCACATTTTCCCCAGTTCAATGCTATGCCAT  
TACCAACTCCAAATAATCTCAAATAATTTTCCACTTAATACTGTAAAGTTTTTTTCTGTTA  
ATTTAGGCATATAGAATATTAAATCTGATATTGCACTTCTTATTTTATATAAAATAATCCT  
TTAATATCCAAATGAATCTGTTAAATGTTTGATTCCCTTGGGAATGGCCTTAAAAATAAATG  
TAATAAAGTCAGAGTGGTGGTATGAAAACATTCTAGTGATCATGTAGTAAATGTAGGGTTA  
AGCATGGACAGCCAGAGCTTTCTATGTACTGTTAAATTTGAGGTCACATATTTTCTTTTGTA  
TCCTGGCAAATACTCCTGCAGGCCAGGAAGTATAATAGCAAAAAGTTGAACAAAGATGAACT  
AATGTATTACATTACCATTGCCACTGATTTTTTTTAAATGGTAAATGACCTTGTATATAAAT  
ATTGCCATATCATGGTACCTATAATGGTGATATATTTGTTTCTATGAAAAATGTATTGTGCT  
TTGATACTAAAAATCTGTAAAAATGTTAGTTTTTGGTAATTTTTTTTCTGCTGGTGGATTTACA  
TATTAAATTTTTTCTGCTGGTGGATAAACATTAAATTAATCATGTTTCAAAAAA

**FIGURE 147**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417

<subunit 1 of 1, 500 aa, 1 stop

<MW: 56888, pI: 8.53, NX(S/T): 2

MKCTAREWLRVTTVLFMARAIPAMVVPNATLLEKLLEKYMDEDGEWWIAKQRGKRAITDNDM  
QSILDLHNKLRSQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNLGAHW  
GRYRPPTFHVQSWYDEVKDFSYPYEHECNFYCPFRCSGPVCTHYTQVWATSNRIGCAINLC  
HNMNIWGQIWPKAVYLVCNYSKGNWWGHAPYKHGRPCSACPPSFGGGCRENLCYKEGSDRY  
YPPREEETNEIERQQSQVHDTHVRTRSDDSSRNEVISAQQMSQIVSCEVRLRDQCKGTTTCNR  
YECPAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITRQGRKHIFYIKSNRNGI  
QTIGKYQSANSFTVSKVTVQAVTCETTVEQLCPFHKPASHCPRVYCPRNCMQANPHYARVIG  
TRVYSDLSSICRAAVHAGVVRNHGGYVDVMPVDKRKTYIASFQNGIFSESLQNPPGGKAFRV  
FAVV

Important features:

Signal peptide:

amino acids 1-20

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

N-glycosylation site

amino acids 28-31

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**FIGURE 148**

GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCG  
CAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGT  
GGCGTCTCCGGGCGCCGCTCCGACGGGGCCAGCGCCCTCCCCATGTCCTGCTCCCACGCCG  
CGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGT  
ACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGTCCCGGAAGGGACCCAAGATCCGCTAC  
AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTTAT  
CATCACCACCAAGAGCGTGTCCAGGTACCGAGGTGAGGAGCACTGCCTGCACCCCAAGCTGC  
AGAGCACCAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGTCTACGAA  
GAATAGGGTGAAAAACCTCAGAAGGGGAAAACCTCCAAACCAGTTGGGAGACTTGTGCAAAGGA  
CTTTGCAGATTAAAAAAGCCTTTC  
TTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTTACCAACGGTCAG  
TTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCCATCTCTCTTGCTGCT  
CCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGGGAAAACCTCATGCCTTTCCTTTTTTAA  
AAAATGCTTTTTTGTATTTGTCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCGGGA  
GGAACAATGAGCTTGGTGGACACATTTCAATTGCAGTGTTGCTCCATTCTAGCTTGGGAAGC  
TTCCGCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCG  
GTCACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCT  
CTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAATGTGCTTCATTCCCCCT  
GGTTAATTTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATC  
CTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTACAGGTTCAATA  
TTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAAC  
TAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAA  
AACCTTCAAAGCATGTTTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATAT  
TTGTGATTCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGAT  
GACCATGCGCCCTTTCCTCTGTACATATACCTTAAGAACGCCCCCTCCACACACTGCCCCC  
CAGTATATGCCGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCAT  
TGCATGCAGGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAA  
AAAAAAAAAA

**FIGURE 149**

MSLLPRRAPPVSMRLLAAALLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPH  
CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNWNEKRRVYEE

**FIGURE 150**

GCCCCAGGGACTGCTATGGCTTCCTTTGTTGTTACCCCCGGTCTGCGTCATGTTAAACTCCA  
ATGTCCTCCTGTGGTTAACTGCTCTTGCCATCAAGTTCACCCTCATTGACAGCCAAGCACAG  
TATCCAGTTGTCAACACAAATTATGGCAAATCCGGGGCCTAAGAACACCGTTACCCAATGA  
GATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCCTATGCCTCACCCCCCACTGGAGAGA  
GGCGGTTTTCAGCCCCCAGAACCCCCGTCTCTGGACTGGCATCCGAAATACTACTCAGTTT  
GCTGCTGTGTGCCCCCAGCACCTGGATGAGAGATCCTTACTGCATGACATGCTGCCCATCTG  
GTTTACCGCCAATTTGGATACTTTGATGACCTATGTTCAAGATCAAAATGAAGACTGCCTTT  
ACTTAAACATCTACGTGCCACGGAAGATGGAGCCAACACAAAGAAAAACGCAGATGATATA  
ACGAGTAATGACCGTGGTGAAGACGAAGATATTCATGATCAGAACAGTAAGAAGCCCGTCAT  
GGTCTATATCCATGGGGGATCTTACATGGAGGGCACCGGCAACATGATTGACGGCAGCATTT  
TGGCAAGCTACGGAAACGTCATCGTGATCACCATTAACCTACCGTCTGGGAATACTAGGGTTT  
TTAAGTACCGGTGACCAGGCAGCAAAAGGCAACTATGGGCTCCTGGATCAGATTCAAGCACT  
GCGGTGGATTGAGGAGAATGTGGGAGCCTTTGGCGGGGACCCCAAGAGAGTGACCATCTTTG  
GCTCGGGGGCTGGGGCCTCCTGTGTGACGCTGTTGACCCTGTCCCACTACTCAGAAGGTCTC  
TTCCAGAAGGCCATCATTGAGAGCGGCACCGCCCTGTCCAGCTGGGCAGTGAAGTACCAGCC  
GGCCAAGTACACTCGGATATTGGCAGACAAGGTGGCTGCAACATGCTGGACACCACGGACA  
TGGTAGAATGCCTGCGGAACAAGAACTACAAGGAGCTCATCCAGCAGACCATCACCCCGGCC  
ACCTACCACATAGCCTTCGGGCGCGGTGATCGACGGCGACGTCATCCAGACGACCCCCAGAT  
CCTGATGGAGCAAGGCGAGTTCCTCAACTACGACATCATGCTGGGCGTCAACCAAGGGGAAG  
GCCTGAAGTTCGTGGACGGCATCGTGGATAACGAGGACGGTGTGACGCCCAACGACTTTGAC  
TTCTCCGTGTCCAACCTTCGTGGACAACCTTTACGGCTACCCTGAAGGGAAAGACACTTTGCG  
GGAGACTATCAAGTTCATGTACACAGACTGGGCGGATAAGGAAAACCCGGAGACGCGGCGGA  
AAACCCTGGTGGCTCTCTTTACTGACCACCAGTGGGTGGCCCCCGCGGTGGCCGCCGACCTG  
CACGCGCAGTACGGCTCCCCACCTACTTCTATGCCTTCTATCATCACTGCCAAAGCGAAAT  
GAAGCCCAGCTGGGCAGATTCGGGCCATGGTGATGAGGTCCCCTATGTCTTCGGCATCCCCA  
TGATCGGTCCCACCGAGCTCTTCAGTTGTAACCTTTTCCAAGAACGACGTCATGCTCAGCGCC  
GTGGTCATGACCTACTGGACGAACTTCGCCAAAACCTGGTGATCCAAATCAACCAGTTCTCTCA  
GGATACCAAGTTCATTACACAAAACCCAACCGCTTTGAAGAAGTGGCCTGGTCCAAGTATA  
ATCCCAAAGACCAGCTCTATCTGCATATTGGCTTGAAACCCAGAGTGAGAGATCACTACCGG  
GCAACGAAAGTGGCTTTCTGGTTGGAACCTCGTTCCTCATTTGCACAACCTGAACGAGATATT  
CCAGTATGTTTCAACAACCACAAAGGTTCTCCACCAGACATGACATCATTTCCCTATGGCA  
CCCGGCGATCTCCCGCCAAGATATGGCCAACCACCAACGCCAGCAATCACTCCTGCCAAC  
AATCCCAAACACTCTAAGGACCCTCACAAAACAGGGCCTGAGGACACAACCTGTCCTCATTGA  
AACCAAACGAGATTATTCCACCGAATTAAGTGTCACCATTGCCGTGCGGGCGTCGCTCCTCT  
TCCTCAACATCTTAGCTTTTGCGGCGCTGTACTACAAAAGGACAAGAGGCGCCATGAGACT  
CACAGGCGCCCCAGTCCCCAGAGAAACACCACAAATGATATCGCTCACATCCAGAACGAAGA  
GATCATGTCTCTGCAGATGAAGCAGCTGGAACACGATCACGAGTGTGAGTCGCTGCAGGCAC  
ACGACACACTGAGGCTCACCTGCCCCGACACTACACCTCACGCTGCGCCGGTCGCCAGAT  
GACATCCCCTTATGACGCCAAACACCATCACCATGATTCCAAACACACTGACGGGGATGCA  
GCCTTTGCACACTTTTAAACACCTTCAGTGGAGGACAAAACAGTACAAATTTACCCACGGAC  
ATTCCACCCTAGAGTATAGCTTTGCCCTATTTCCCTTCTCTATCCCTCTGCCCTACCCGCTC  
AGCAACATAGAAGAGGGGAAGGAAAGAGAGAAGGAAAGAGAGAGAGAAAGAAAGTCTCCAGAC  
CAGGAATGTTTTTGTCCCACTGACTTAAGACAAAATGCAAAAAGGCAGTCATCCCATCCCG  
GCAGACCCTTATCGTTGGTGTGTTTCCAGTATTACAAGATCAACTTCTGACCCTGTGAAATGT  
GAGAAGTACACATTTCTGTAAAATAACTGCTTTAAGATCTCTACCACTCCAATCAATGTTT  
AGTGTGATAGGACATCACCATTTCAAGGCCCCGGGTGTTTCCAACGTCATGGAAGCAGCTGA  
CACTTCTGAACTCAGCCAAGGACACTTGATATTTTTTAATTACAATGGAAGTTTAAACATT  
TCTTTCTGTGCCACACAATGGATGGCTCTCCTTAAGTGAAGAAAGAGTCAATGAGATTTTGC  
CCAGCACATGGAGCTGTAATCCAGAGAGAAGGAAACGTAGAAATTTATTATTAAAGAATGG  
ACTGTGCAGCGAAATCTGTACGGTTCTGTGCAAAGAGGTGTTTTGCCAGCCTGAACTATATT  
TAAGAGACTTTGT



**FIGURE 151**

MLNSNVLLWLTALAIKFTLIDSQAQYPVVNTNYGKIRGLRTPLPNEILGPVEQYLGVPYASP  
PTGERRFQPPEPPSSWTGIRNTTQFAAVCPQHLDERSLLHDMPLIWFTANLDTLMTYVQDQN  
EDCLYLNIYVPTEDGANTKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI  
DGSILASYGNVIVITINYRLGILGFLSTGDQAAKGNYGLLDQIQALRWIEENVGAFGGDPKR  
VTIFGSGAGASCVSLLTSLHYSEGLFQKAI IQSGTALSSWAVNYQPAKYTRILADKVGCMNL  
DTTDMVECLRNKNYKELIQQTITPATYHIAFGPVIDGDVIPDDPQILMEQGEFLNYDIMLGV  
NQGEGLKFVDGIVDNEDGVTPNDFDFSVSNFVDNLYGYPEGKDTLRET IKFMYTDWADKENP  
ETRRKTLVALETDHQWVAPAVAADLHAQYGSPTYFYAFYHHCQSEMKP SWADSAHGDEVPIYV  
FGIPMIGPTELFSCNFSKNDVMLS AVVM TYWTNFAKTGDPNQVPQDTKFIHTKPNRFEEVA  
WSKYNPKDQLYLHIGLKPRVRDHYRATKVAFWLELVPHLHNLNEIFQYVSTTTKVPPDMTS  
FPYGTRRSPAKIWPTTKRPAITPANNPKH SKDPHKTGPEDTTVLIETKRDYSTE LSVTI AVG  
ASLLFLNILAFAALYYKKDKRRHETHRRPSQORNTTNDIAHIQNEEIMSLQMKQLEHDHECE  
SLQAHDTLRLTCPPDYTLTLRRSPDDIPLMTPNTITMIPNTLTGMQPLHTFNTFSGGQNSTN  
LPHGHSTTRV

**FIGURE 152**

GGGAAAGATGGCGGCGACTCTGGGACCCCTTGGGTCTGGCAGCAGTGGCGGCGATGTTTGT  
CGGCTCGGGATGGGTCCAGGATGTTACTCCTTCTTCTTTTGTGGGGTCTGGGCAGGGGCCA  
CAGCAAGTCGGGGCGGGTCAAACGTTTCGAGTACTTGAAACGGGAGCACTCGCTGTGGAAGCC  
CTACCAGGGTGTGGGCACAGGCAGTTCCTCACTGTGGAATCTGATGGGCAATGCCATGGTGA  
TGACCCAGTATATCCGCCTTACCCAGATATGCAAAGTAAACAGGGTGCCTTGTGGAACCGG  
GTGCCATGTTTCTGAGAGACTGGGAGTTGCAGGTGCACTTCAAAATCCATGGACAAGGAAA  
GAAGAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGGC  
CTGTGTTTGGAAACATGGACAAATTTGTGGGGCTGGGAGTATTTGTAGACACCTACCCCAAT  
GAGGAGAAGCAGCAAGAGCGGGTATTCCCCTACATCTCAGCCATGGTGAACAACGGCTCCCT  
CAGCTATGATCATGAGCGGGATGGGCGGCCTACAGAGCTGGGAGGCTGCACAGCCATTGTCC  
GCAATCTTCATTACGACACCTTCTGGTGATTCTGCTACGTCAAGAGGCATTTGACGATAATG  
ATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCGGAGTCCGCCTGCC  
CCGCGGCTACTACTTCGGCACCTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCA  
TTTCCTTGAAGTTGTTTGAAGTGCAGTGGAGAGAACCCAGAAAGAGGAAAAGCTCCATCGA  
GATGTGTTCTTGCCCTCAGTGGACAATATGAAGCTGCCTGAGATGACAGCTCCACTGCCGCC  
CCTGAGTGGCCTGGCCCTCTTCCTCATCGTCTTTTTCTCCCTGGTGTCTTCTGTATTTGCCA  
TAGTCATTGGTATCATACTCTAGAACAATGGCAGGAACAGAGCCGAAAGCGCTTCTACTGA  
GCCCTCCTGCTGCCACCACTTTTGTGACTGTCACCCATGAGGTATGGAAGGAGCAGGCACTG  
GCCTGAGCATGCAGCCTGGAGAGTGTCTTGTCTCTAGCAGCTGGTTGGGGACTATATTCTG  
TCACTGGAGTTTTGAATGCAGGGACCCCGCATTTCCCATGGTTGTGCATGGGGACATCTAACT  
CTGGTCTGGGAAGCCACCCACCCAGGGCAATGCTGCTGTGATGTGCCTTTCCCTGCAGTCC  
TTCCATGTGGGAGCAGAGGTGTGAAGAGAATTTACGTGGTTGTGATGCCAAAATCACAGAAC  
AGAATTTCATAGCCCAGGCTGCCGTGTTGTTTGAAGTGCAGAGGCCCCTTCTACTTCAGTTTTG  
AATCCACAAAGAATTAAAACTGGTAACACCACAGGCTTTCTGACCATCCATTTCGTTGGGTT  
TTGCATTTGACCCAACCCTCTGCCTACCTGAGGAGCTTTCTTTGGAAACCAGGATGGAACT  
TCTTCCCTGCCTTACCTTCTTTCACTCCATTCAATTGTCTCTGTGTGCAACCTGAGCTG  
GGAAAGGCATTTGGATGCCTCTCTGTTGGGGCCTGGGGCTGCAGAACACACCTGCGTTTCAC  
TGGCCTTCATTAGGTGGCCCTAGGGAGATGGCTTTCTGCTTTGGATCACTGTTCCCTAGCAT  
GGGTCTTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTCTTCAGGCCCTCAGTG  
AAGTTTGGCTAAAGGTTGGTGTAAAAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATG  
GATTAGCTGTGCAACTGACCAGCTCCAGGTTTGATCAAACCAAAGCAACATTTGTCATGTG  
GTCTGACCATGTGGAGATGTTTCTGGACTTGCTAGAGCCTGCTTAGCTGCATGTTTTGTAGT  
TACGATTTTTGGAATCCCACTTTGAGTGCTGAAAGTGTAAGGAAGCTTTCTTCTTACACCTT  
GGGCTTGGATATTGCCAGAGAAGAAATTTGGCTTTTTTTTTCTTAATGGACAAGAGACAGT  
TGCTGTTCTCATGTTCCAAGTCTGAGAGCAACAGACCCTCATCATCTGTGCCTGGAAGAGTT  
CACTGTCATTGAGCAGCACAGCCTGAGTGCTGGCCTCTGTCAACCCTTATTCCTACTGCCTTA  
TTTGACAAGGGGTACATGCTGCTCACCTTACTGCCCTGGGATTAAATCAGTTACAGGCCAG  
AGTCTCCTTGGAGGGCCTGGAACCTCTGAGTCCTCCTATGAACCTCTGTAGCCTAAATGAAAT  
TCTTAAATCACCGATGGAACCAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCG  
ACCTGCAGTAGGGATAACAGGGTAATAAGCTTGGCCGCCATGG



**FIGURE 153**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911  
><subunit 1 of 1, 348 aa, 1 stop  
><MW: 39711, pI: 8.70, NX(S/T): 1  
MAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLLGSGQGPGQVGAGQTFEYLKREHSLSKPYQ  
GVGTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQALWNRVPCFLRDWELQVHFKEHGQKKN  
LHGDGLAIWYTKDRMQPGPVFGNMDKFVGLGVFVDTPNEEKQOQERVFPYISAMVNNGSLSY  
DHERDGRPTELGGCTAIVRNLYHDTFLVIRYVKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG  
YYFGTSSITGDLSDNHDTVSLKLFELTVERTPEEEKLHRDVFLPSVDNMKLPENTAPLPPLS  
GLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKRFY

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**FIGURE 154**

CCGAGCCGGGCGCGCAGCGACGGAGCTGGGGCCGGCCTGGGACCATGGGCGTGAGTGCAATC  
TACGGATCAGTCTCTGATGGTGGGTCGTTAACCTCAGTGGGGACTCCAAGATTTCCATGAAG  
AAAATCAGTTGTCTTCATTCAAGAATTGGGGTCTGGCTCAGAATTCCTGCAGCTGGTGAAAA  
TCTGTTTTCTAGAAGAGGTTTAAATTAATGCCTGCAGTCTGACATGTTCCCGATTTGAGGTGA  
AACCATGAAGAGAAAAATAGAATACTTAATAATGCTTTTCCGCAACCGCTTCTTGCTGCTGCT  
GGCCCTGGCTGCGCTGCTGGCCTTTGTGAGCCTCAGCCTGCAGTTCTTCCACCTGATCCCGG  
TGTCGACTCCTAAGAATGGAATGAGTAGCAAGAGTCGAAAGAGAATCATGCCCGACCCCTGTG  
ACGGAGCCCCCTGTGACAGACCCCGTTTATGAAGCTCTTTTGTACTGCAACATCCCCAGTGT  
GGCCGAGCGCAGCATGGAAGGTCATGCCCCGCATCATTTTAAGCTGGTCTCAGTGCATGTGT  
TCATTCGCCACGGAGACAGGTACCCACTGTATGTCATTCCCAAACAAAGCGACCAGAAATT  
GACTGCACTCTGGTGGCTAACAGGAAACCGTATCACCCAAACTGGAAGCTTTCATTAGTCA  
CATGTCAAAGGATCCGGAGCCTCTTTCGAAAGCCCCCTTGAACCTCTTGCTCTTTACCCAA  
ATCACCCATTGTGTGAGATGGGAGAGCTCACACAGACAGGAGTTGTGCAGCATTTGCAGAAC  
GGTCAGCTGCTGAGGGATATCTATCTAAAGAAACACAAACTCCTGCCCAATGATTGGTCTGC  
AGACCAGCTCTATTTAGAGACCACTGGGAAAAGCCGGACCCTACAAAGTGGGCTGGCCTTGC  
TTTATGGCTTTCTCCCAGATTTTGTACTGGAAGAAGATTTATTTTCAGGCACCAGCCAAGTGC  
CTGTTCTGCTCTGGAAGCTGCTATTGCCCGGTAAGAAACCAGTATCTGGAAAAGGAGCAGCG  
TCGTGAGTACCTCCTACGTTTGAAAAACAGCCAGCTGGAGAAGACCTACGGGGAGATGGCCA  
AGATCGTGGATGTCCCCACCAAGCAGCTTAGAGCTGCCAACCCCATAGACTCCATGCTCTGC  
CACTTCTGCCACAATGTCAGCTTTCCTGTACCAGAAATGGCTGTGTTGACATGGAGCACTT  
CAAGGTAATTAAGACCCATCAGATCGAGGATGAAAGGGAAAGACGGGAGAAGAAATTGTACT  
TCGGGTATTCTCTCCTGGGTGCCACCCCATCCTGAACCAAACCATCGGCCGGATGCAGCGT  
GCCACCGAGGGCAGGAAAGAAGAGCTCTTTGCCCTCTACTCTGCTCATGATGTCACTCTGTC  
ACCAGTTCTCAGTGCCTTGGGCCTTTCAGAAGCCAGGTTCCCAAGGTTTGCAGCCAGGTTGA  
TCTTTGAGCTTTGGCAAGACAGAGAAAAGCCCAGTGAACATTCCGTCCGGATTCTTTACAAT  
GGCGTCGATGTCACATTCCACACCTCTTTCTGCCAAGACCACCACAAGCGTTCTCCCAAGCC  
CATGTGCCCGCTTGAAAACCTTGGTCCGCTTTGTGAAAAGGGACATGTTTGTAGCCCTGGGTG  
GCAGTGGTACAAATTATTATGATGCATGTCACAGGGAAGGATTCTAAAAGGTATGCAGTACA  
GCAGTATAGAATCCATGCCAATACAGAGCATAGGGAAAGGTCCACTTCTAGTTTTTGTCTGTT  
ACTAAGGGTAGAAGATTATTGCTTTTTTAAAGGCTAAATATTGTTTGTGGGAACCACAGATGG  
TTGGGGTTGAACAGTAAGCACATTGCTGCAATGTGGTACGTGAATTGCTTGGTACAAAATGG  
CCAGTTCACAGAGGAATAGAAGGTACTTTATCATAGCCAGACTTCGCTTAGAATGCCAGAAT  
AATATAGTTCAAGACCTGAAGTTGCCAATCCAAGTTTGCAGTCTTCTGGCCTGCCCCATGTT  
ACTATGTGATGGAACCAGCACACCTCAACCAAATTTTTTTAATCTTAGACATTTTTTACCTT  
GTCCTTGTTAAGAATTTCTTGAAGTGATTTATCTAAAATAAAGGTTGGCAAACCTTTTTCTGT  
AAAGGGCCAGATTGTAAATATTTTCAGACTGTGTGGACCAAAGGCCACATACAGTCTCTGTC  
ATAACTACTCAACTCTGTTTCTGAAGCAGGAAAGCCACCACAGACAGTACATAAAGGAATAT  
GTGTAGCTGGGTTCACAGGCCAGACAAAACAGATGGTGACCAGACTTGGCCCCCTGGGCTGTA  
GTTTGCTGACCCCTCATCTAAAAAATAGGCTATACTACAATTGCACTTCCAGCACTTTGAGA  
ACGAGTTGAATACCAAGAATTATTCAATGGTTCCTCCAGTAACTTCTGCTAGAAACACAGAA  
TTTGGTCTGTATCTGACACTAGAACAAAACCTTGAGGGTAAATAAACATTGAATTAGAATGAA  
TCATAGAAAACCTGATTAGAAGAATACTTGATGTTTATGATGATTGTGGTACAAGATAGTTTT  
AAGTATGTTCTAAATATTTGTCTGCTGTAGTCTATTTGCTGTATATGCTGAAATTTTTGTAT  
GCCATTTAGTATTTTTTATAGTTTAGGAAAATATTTTCTAAGACCAGTTTTAGATGACTCTTA  
TTCTGTAGTAATATTCAATTTGCTGTACCTGCTTGGTGGTTAGAAGGAGGCTAGAAGATGA  
ATTCAGGCACCTTTCTTCCAATAAACTAATTATGGCTCATTCCTTTGACAAGCTGTAGAAC  
TGGATTCATTTTTAAACCATTTTCATCAGTTTCAAATGGTAAATTCTGATTGATTTTTAAAT  
GCGTTTTTGGAGAAGCTTTGCTATTAGGTAGTTTACAGATCTTTATAAGGTGTTTTATATAT  
TAGAAGCAATTATAATTACATCTGTGATTTCTGAACATAATGGTGCTAATTCAGAGAAATGGA  
AAGTGAAAGTGAGATTCTCTGTTGTCATCGGCATTCCAACCTTTTCTCTTTGTTTTGTCCA  
GTGTTGCATTTGAATATGTCTGTTTCTATAAAATAAATTTTTTAAGAATAA

**FIGURE 155**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329  
><subunit 1 of 1, 480 aa, 1 stop  
><MW: 55240, pI: 9.30, NX(S/T): 2  
MLFRNRFLLLLALAAALLAFVSLSLQFFHLIPVSTPKNGMSSSKSRKRIMPDVPVTEPPVTDVPVY  
EALLYCNIPPSVAERSMEGHAPHHFKLVSVHVFIRHGDRYPLYVIPKTKRPEIDCTLVANRKP  
YHPKLEAFISHMSKSGSGASFESPLNSLPLYPNHPLCEMGELTQTGVVQHLQNGQLLRDIYLYK  
KHKLLPNDWSADQLYLETTGKSRTLQSGLALLYGFLPDFDWKKIYFRHQPSALFCSGSCYCP  
VRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSMMLCHFCHNVSFPC  
TRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSLLGAHPILNQTIGRMQRATEGRKEELF  
ALYSAHDVTLSPVLSALGLSEARFPRFAARLIFELWQDREKPSSEHSVRILYNGVDVTFHTSF  
CQDHHKRSPKPMCPLENLVRVFKRDMFVALGGSGTNYYDACHREGF

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AAAAAAGCTCACTAAAGTTTCTATTAGAGCGAATACGGTAGATTTCCATCCCCCTTTTGAAGA  
ACAGTACTGTGGAGCTATTTAAGAGATAAAAACGAAATATCCTTTCTGGGAGTTCAAGATTG  
TGCAGTAATTGGTTAGGACTCTGAGCGCCGCTGTTACCAATCGGGGAGAGAAAAGCGGAGA  
TCCTGCTCGCCTTGACGCGCCTGAAGCACAAAGCAGATAGCTAGGAATGAACCATCCCTGG  
GAGTATGTGGAAACAACGGAGGAGCTCTGACTTCCCAACTGTCCCATTCTATGGGCGAAGGA  
ACTGCTCCTGACTTCAGTGGTTAAGGGCAGAATTGAAAATAATTCTGGAGGAAGATAAGAAAT  
GATTCTCTGCGCGACTGCACCGGGACTACAAAGGGCTTGTCTGCTGGGAATCCTCCTGGGGA  
CTCTGTGGGAGACCGGATGCACCCAGATACGCTATTAGTTCCGGAAGAGCTGGAGAAAGGC  
TCTAGGGTGGGCGACATCTCCAGGGACCTGGGGCTGGAGCCCCGGGAGCTCGCGGAGCGCGG  
AGTCCGCATCATCCCCAGAGGTAGGACGCGAGCTTTTCGCCCTGAATCCGCGCAGCGGCAGCT  
TGGTCACGGCGGGCAGGATAGACCGGGAGGAGCTCTGTATGGGGGCCATCAAGTGTCAATTA  
AATCTAGACATTCTGATGGAGGATAAAGTGAAAATATATGGAGTAGAAGTAGAAGTAAGGGA  
CATTAACGACAATGCGCCTTACTTTCTGTGAAAGTGAATTAGAAATAAAAATTAGTGAAAATG  
CAGCCACTGAGATGCGGTTCCCTCTACCCACGCTTGGGATCCGGATATCGGGAAGAACTCT  
CTGCAGAGCTACGAGCTCAGCCCGAACACTCACTTCTCCCTCATCGTGCAAAATGGAGCCGA  
CGGTAGTAAGTACCCCGAATTGGTGCTGAAACGCGCCCTGGACCGCGAAGAAAAGGCTGCTC  
ACCACCTGGTCTTACGGCCTCCGACGGGGGCGACCCGGTGCGCACAGGCACCGCGCGCATC  
CGCGTGATGGTTCTGGATGCGAACGACAACGACACGCGTTTGCTCAGCCCGAGTACCGCGC  
GAGCGTTCCGGAGAATCTGGCCTTGGGCACGCGAGCTGCTTGTAGTCAACGCTACCGACCCCTG  
ACGAAGGAGTCAATGCGGAAGTGAGGTATTCTTCCGGTATGTGGACGACAAGGCGGCCCAA  
GTTTTCAAAC TAGATTGTAATTCAGGGACAATATCAACAATAGGGGAGTTGGACCACGAGGA  
GTCAGGATTCTACCAGATGGAAGTGCAAGCAATGGATAATGCAGGATATTCTGCGCGAGCCA  
AAGTCTTGATCACTGTTCTGGACGTGAACGACAATGCCCCAGAAGTGGTCTCACCTCTCTC  
GCCAGCTCGGTCCCCGAAAACCTCTCCAGAGGGACATTAATTGCCCTTTTAAATGTAAATGA  
CCAAGATTCTGAGGAAAACGGACAGGTGATCTGTTTCATCCAAGGAAATCTGCCCTTTAAAT  
TAGAAAAATCTTACGGAAATTACTATAGTTTAGTCACAGACATAGTCTTGGATAGGGAACAG  
GTTCTTAGCTACAACATCACAGTGACCGCCACTGACCGGGGAACCCCGCCCCCTATCCACGGA  
AACTCATATCTCGCTGAACGTGGCAGACACCAACGACAACCCGCGCGGTCTTCCCTCAGGCCT  
CCTATTCCGCTTATATCCCAGAGAACAATCCCAGAGGAGTTTCCCTCGTCTCTGTGACCGCC  
CACGACCCCGACTGTGAAGAGAACGCCCAGATCACTTATTCCCTGGCTGAGAACACCATCCA  
AGGGGCAAGCCTATCGTCTTACGTGTCCATCAACTCCGACACTGGGGTACTGTATGCGCTGA  
GCTCCTTCGACTACGAGCAGTTCCGAGACTTGCAAGTGAAAGTGATGGCGCGGGACAACGGG  
CACCCGCCCCCTCAGCAGCAACGTGTCTGTTGAGCCTGTTCTGTGCTGGACCAGAACGACAATGC  
GCCCCGAGATCCTGTACCCCGCCCTCCCCACGGACGGTTCCACTGGCGTGGAGCTGGCTCCCC  
GCTCCGCAGAGCCCGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACAGAGACTCCGGCCAG  
AACGCCTGGCTGTCTTACCGTCTGCTCAAGGCCAGCGAGCCGGGACTCTTCTCGGTGGGTCT  
GCACACGGGCGAGGTGCGCACGGCGCGAGCCCTGCTGGACAGAGACGCGCTCAAGCAGAGCC  
TCGTAGTGGCCGTCCAGGACCACGGCCAGCCCCCTCTCTCCGCCACTGTACGCTCACCGTG  
GCCGTGGCCGACAGCATCCCCCAAGTCTTGGCGGACCTCGGCAGCCTCGAGTCTCCAGCTAA  
CTCTGAAACCTCAGACCTCACTCTGTACCTGGTGGTAGCGGTGGCCGCGGTCTCCTGCGTCT  
TCCTGGCCTTCGTCTCTTGTGCTGCTGGCGCTCAGGCTGCGGCGCTGGCACAAGTCACGCCTG  
CTGCAGGCTTCAGGAGGCGGCTTGACAGGAGCGCCGGCGTGCAGCTTTGTGGGCGTGGACGG  
GGTGCAGGCTTTCTGCGAGACCTATTCCACGAGGTTTCCCTCACCACGGACTCGCGGAAGA  
GTCACCTGATCTTCCCCCAGCCCAACTATGCAGACATGCTCGTCAGCCAGGAGAGCTTTGAA  
AAAAGCGAGCCCCCTTTTGCTGTGAGGTGATTGGGTATTTTCTAAAGACAGTCATGGGTAAAT  
TGAGGTGAGTTTATATCAAATCTTCTTTCTTTTTTTTTTTTAAATTGCTCTGTCTCCCAAGCTG  
GAGTGCAGCGGTACGATCATAGCTCACTGCGGCCTCAAACCTCTAGGCTCAAGCAATTATCC  
CACCTTTGCCTCCGGTGTAACAGGGACTACAGGTGCAAGCCACCTACTGTCTGCCTATCTAT  
CTATCTATCTATCTATCTATCTATCTATCTATCTATCTATTACTTTCTTGTACAGACG  
GGAGTCTCACGCCTGTAATCCCAGTACTTTGGGAGGCCGAGGCGGGTGGATCACCTGAGGTT  
GGGAGTTTGAGACCAGCCTGACCAACATGGAGAAACCCCGTCTATACTAAAAAATAACAAA  
TTAGCCGGGCGTGGTGGTGCATGTCTGTAATCCCAGCTACTTGGGAGGCTGAGTCAGGAGAA  
TTGCTTTAACTGGGAGGTGGAGGTTGCAATGAGCTGAGATTGTGCCATTGCACTCCAGCCT  
GGGCAACAAGAGTGAAACTCTATCTCA

**FIGURE 157**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306  
><subunit 1 of 1, 916 aa, 1 stop  
><MW: 100204, pI: 4.92, NX(S/T): 4  
MIPARLHRDYKGLVLLGILLGTLWETGCTQIRYSVPEELEKGSRVGDISRDLGLEPRELAER  
GVRIIPRGRTQLFALNPRSGSLVTAGRIDREELCMGAIKCQLNLDILMEDKVKIYGVEVEVR  
DINDNAPYFRESELEIKISENAATEMRFPPLPHAWDPDIGKNSLQSYELSPNTHESLIVQNGA  
DGSKYPELVVKRALDREEKAAHHLVLTASDGGDPVRTGTARIRVMVLDANDNAPAFAPQPEYR  
ASVPENLALGTQLLVVNATDPDEGVNAEVRYSEFRYVDDKAAQVFKLDCNSGTISTIGELDHE  
ESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTSASSVPENSPRGTLIALLNVN  
DQDSEENGQVICFIQGNLPFKLEKSYGNYSLVTDIVLDREQVPSYNITVTATDRGTPPLST  
ETHISLNVADTNDNPPVFPQASYSAYIPENNPRGVSLVSVTAHDPDCEENAQITYSLAENTI  
QGASLSSYVSINSDTGVLIALSSFDYEQFRDLQVKVMARDNGHPPLSSNVSLSLFVLDQNDN  
APEILYPALPTDGSTGVELAPRSAEPGYLVTKVVAVDRDSGQNAWLSYRLLKASEPGLFSVG  
LHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTTLTVAVADSIPQVLADLGSLESPA  
NSETSDLTLYLVVAVAAVSCVFLAFVILLALLRLRRWHKSRLLQASGGGLTGAPASHFVGVD  
GVQAFLQTYSHVSLTTDSRKSHLIFPQPNYADMLVSQESFEKSEPLLLSGDSVFSKDSHGL  
IEVSLYQIFFLFFFNCSVSQAGVQRYDHSSLRPQTPRLKQLSHLCLRCNRDYRCKPPTVCLS  
IYLSIYLSIYLSIYLLLSCTDGSLTPVIPVLWEAEAGGSPEVGSLRPA



**FIGURE 158**

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAG  
GCTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAA  
TCAGTAGGTGACCCCGCCCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCCGACCTCGT  
GCGGCCAAGACGTGGATGTTCTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGC  
ACAGGAGGACAAGGTGCTGGGGGGTTCATGAGTGCCAACCCCATTCGCAGCCTTGGCAGGCGG  
CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAAGGTGGCAACTGGGTCTT  
ACAGCTGCCCCACTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAA  
TAAAGATGGCCCAGAGCAAGAAATACCTGTGGTTCAGTCCATCCCACACCCCTGCTACAACA  
GCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCC  
CTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTG  
CACCGTCTCAGGCTGGGGCACTGTCACCAGTCCCCGAGAGAATTTTCCTGACACTCTCAACT  
GTGCAGAAGTAAAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACA  
GATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGG  
CCCCCTGGTGTGTGATGGTGCACCTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGA  
GGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATC  
ATAGGCAGCAAGGGCTGATTTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACTCT  
CTGGTTC

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**FIGURE 159**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336  
<subunit 1 of 1, 260 aa, 1 stop  
<MW: 28048, pI: 7.87, NX(S/T): 1  
MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVL  
VGGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEI PVVQSI PHPCYNSSDVEDHNDLMLL  
QLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFDTLNCAEVKIFPQKKCED  
AYPGQITDGMVCAGSSKGADTCQGDGGPLVCDGALQGITSWGS DPCGRSDKPGVYTNICRY  
LDWIKKIIGSKG

**Important Features:****Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 51-71

**N-glycosylation site.**

amino acids 110-113

**Serine proteases, trypsin family, histidine active site.**

amino acids 69-74 and 207-217

**Tyrosine kinase phosphorylation site.**

amino acids 182-188

**Kringle domain proteins motif**

amino acids 205-217

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**FIGURE 160**

GGCGCCGGTGCACCGGGCGGGCTGAGCGCCTCCTGCGGGCCCGGCCTGCGCGCCCCGGCCCCG  
CGCGCCGCCCCACGCCCCAACCCCGGCCCCGCGCCCCCTAGCCCCCGCCCGGGCCCCGCGCCCCG  
GCCCCGCGCCAGGTGAGCGCTCCGCCCCGCGCGAGGCCCCGCCCCGGCCCCGCCCCCGCCCCG  
CCCCGGCCGGCGGGGGAACCGGGCGGATTCTCTCGCGCGTCAAACACCTGATCCCATAAAC  
ATTTCATCCTCCCGGCGGCCCCGCGCTGCGAGCGCCCCGCCAGTCCGCGCCGCGCGCCGCTCG  
CCCTGTGCGCCCTGCGCGCCCTGCGCACCCGCGGCCCCGAGCCCAGCCAGAGCCGGGCGGAGC  
GGAGCGCGCCGAGCCTCGTCCCGCGGCCGGGCGGGGCCGGGCGTAGCGGCGGCGCCTGGA  
TGCGGACCCGGCCGCGGGGAGACGGGCGCCCCGCCCGAAACGACTTTCAGTCCCCGACGCGC  
CCCGCCCCAACCCCTACGATGAAGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTG  
CTGTGGCTGCGAGGCTGGCAGGTGGCAGCCCCATGCCAGGTGCCTGCGTATGCTACAATGA  
GCCCCAAGGTGACGACAAGCTGCCCCCAGCAGGGCCTGCAGGCTGTGCCCGTGGGCATCCCTG  
CTGCCAGCCAGCGCATCTTCCTGCACGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTC  
CGTGCCCTGCCGCAACCTCACCATCCTGTGGCTGCACTCGAATGTGCTGGCCCCGAATTGATGC  
GGCTGCCCTTCACTGGCCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCC  
GGTCTGTGGACCCTGCCACATTCCACGGCCTGGGCGCCTACACACGCTGCACCTGGACCGC  
TGCGGCCTGCAGGAGCTGGGCCCCGGGGCTGTTCCGCGGCCTGGCTGCCCTGCAGTACCTCTA  
CCTGCAGGACAACGCGCTGCAGGCACTGCCTGATGACACCTTCCGCGACCTGGGCAACCTCA  
CACACCTCTTCCTGCACGGCAACCGCATCTCCAGCGTGCCCCGAGCGCGCCTTCCGTGGGCTG  
CACAGCCTCGACCGTCTCCTACTGCACCAGAACC GCGTGGCCCATGTGCACCCGCATGCCTT  
CCGTGACCTTGGCCGCTCATGACACTCTATCTGTTTGCCAACAATCTATCAGCGCTGCCCA  
CTGAGGCCCTGGCCCCCTGCGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTG  
TGTGACTGCCGGGCACGCCCCACTCTGGGCCTGGCTGCAGAAGTTCCGCGGCTCCTCCTCCGA  
GGTGCCCTGCAGCCTCCCGCAACGCTGGCTGGCCGTGACCTCAAACGCTAGCTGCCAATG  
ACCTGCAGGGCTGCGCTGTGGCCACCGGCCCTTACCATCCCATCTGGACCGGCAGGGCCACC  
GATGAGGAGCCGCTGGGGCTTCCCAAGTGCTGCCAGCCAGATGCCGCTGACAAGGCCTCAGT  
ACTGGAGCCTGGAAGACCAGCTTCGGCAGGCAATGCGCTGAAGGGACGCGTGCCGCCCCGGTG  
ACAGCCCCGCCGGGCAACGGCTCTGGCCCACGGCACATCAATGACTCACCCCTTTGGGACTCTG  
CCTGGCTCTGCTGAGCCCCCGCTCACTGCAGTGCGGCCCCGAGGGCTCCGAGCCACCAGGGTT  
CCCCACCTCGGGCCCTCGCCGGAGGCCAGGCTGTTACGCAAGAACCGCACCCGCGAGCCACT  
GCCGTCTGGGCCAGGCAGGCAGCGGGGGTGGCGGGACTGGTGACTCAGAAGGCTCAGGTGCC  
CTACCCAGCCTCACCTGCAGCCTCACCCCCCTGGGCCTGGCGCTGGTGCTGTGGACAGTGCT  
TGGGCCCTGCTGAACCCCCAGCGGACACAAGAGCGTGCTCAGCAGCCAGGTGTGTGTACATAC  
GGGGTCTCTCTCCACGCCGCCAAGCCAGCCGGGCGGCCGACCCGTGGGGCAGGCCAGGCCAG  
GTCCTCCCTGATGGACGCCTGCCGCCCCGCCACCCCATCTCCACCCCATCATGTTTACAGGG  
TTCGGCGGCAGCGTTTGTTCAGAACGCCGCTCCACCCAGATCGCGGTATATAGAGATAT  
GCATTTTATTTTACTTGTGTAAAAATATCGGACGACGTGGAATAAAGAGCTCTTTTCTTAAA  
AAAA

**FIGURE 161**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184  
><subunit 1 of 1, 473 aa, 1 stop  
><MW: 50708, pI: 9.28, NX(S/T): 6  
MKRASAGGSRL LAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCFQQGLQAVPVGIPAASQRI  
FLHGNRISHVPAASFRACRNLTILWLHSNVLARIDAAFTGLALLEQLDLSDNAQLRSVDPA  
TFHGLGRLHTLHLDRCGLQELGPGLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLH  
GNRISSVPERAFRGLHSLDRLLLHQNRVAHVHPHAFRDLGRLMTLYLFANNLSALPTEALAP  
LRALQYLRLNDNPWVCDRCRARPLWAWLQKFRGSSSEVPCLPQRLAGRDLKRLAANDLOGCA  
VATGPYHPIWTGRATDEEPLGLPKCCQPDADKASVLEPGRPASAGNALKGRVPPGDSPPGN  
GSGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQA  
GSGGGGTGDSEGGALPSLTCSLTPLGLALVLWTVLGPC

Important features:

Signal peptide:

amino acids 1-26

Leucine zipper pattern.

amino acids 135-156

Glycosaminoglycan attachment site.

amino acids 436-439

N-glycosylation site.

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

VWFC domain

amino acids 411-425

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**FIGURE 162**

GGAAGTCCACGGGGAGCTTGGATGCCAAAGGGAGGACGGCTGGGTCTCTGGAGAGGACTAC  
TCACTGGCATATTTCTGAGGTATCTGTAGAATAACCACAGCCTCAGATACTGGGGACTTTAC  
AGTCCCACAGAACCGTCCTCCCAGGAAGCTGAATCCAGCAAGAACAATGGAGGCCAGCGGGA  
AGCTCATTTGCAGACAAAGGCAAGTCCTTTTTTCTCTTTTGGGCTTATCTCTGGCG  
GGCGCGGCGGAACCTAGAAGCTATTCTGTGGTGGAGGAACTGAGGGCAGCTCCTTTGTCAC  
CAATTTAGCAAAGGACCTGGGTCTGGAGCAGAGGGAATTCTCCAGGCGGGGGGTTAGGGTTG  
TTTCCAGAGGGGAACAACTACATTTGCAGCTCAATCAGGAGACCGCGGATTTGTTGCTAAAT  
GAGAAATTGGACCGTGAGGATCTGTGCGGTACACAGAGCCCTGTGTGCTACGTTTCCAAGT  
GTTGCTAGAGAGTCCCTTCGAGTTTTTTCAAGCTGAGCTGCAAGTAATAGACATAAACGACC  
ACTCTCCAGTATTTCTGGACAAACAAATGTTGGTGAAAGTATCAGAGAGCAGTCCTCCTGGG  
ACTACGTTTCTCTGAAGAATGCCGAAGACTTAGATGTAGGCCAAAACAATATTGAGAACTA  
TATAATCAGCCCCAACTCCTATTTTCGGGTCTCACCCGCAAACGCAGTGATGGCAGGAAAT  
ACCCAGAGCTGGTGCTGGACAAAGCGCTGGACCGAGAGGAAGAAGCTGAGCTCAGGTTAACA  
CTCACAGCACTGGATGGTGGCTCTCCGCCCAGATCTGGCACTGCTCAGGTCTACATCGAAGT  
CCTGGATGTCAACGATAATGCCCCCTGAATTTGAGCAGCCTTTCTATAGAGTGCAGATCTCTG  
AGGACAGTCCGGTAGGCTTCCTGGTTGTGAAGGTCTCTGCCACGGATGTAGACACAGGAGTC  
AACGGAGAGATTTCTATTCACTTTTCCAAGCTTCAGAAGAGATTGGCAAACCTTTAAGAT  
CAATCCCTTGACAGGAGAAATTGAACTAAAAAAACAACCTCGATTTGAAAAACTTCAGTCCT  
ATGAAGTCAATATTGAGGCAAGAGATGCTGGAACCTTTTCTGGAAAATGCACCGTTCTGATT  
CAAGTGATAGATGTGAACGACCATGCCCCAGAAGTTACCATGTCTGCATTTACCAGCCCAAT  
ACCTGAGAACGCGCCTGAAACTGTGGTTGCACTTTTCAGTGTTTCAGATCTTGATTACAGGAG  
AAAATGGGAAAATTAGTTGCTCCATTCAGGAGGATCTACCCTTCCTCCTGAAATCCGCGGAA  
AACTTTTACACCCTACTAACGGAGAGACCCTAGACAGAGAAAGCAGAGCGGAATACAACAT  
CACTATCACTGTCACTGACTTGGGGACCCCTATGCTGATAACACAGCTCAATATGACCGTGC  
TGATCGCCGATGTCAATGACAACGCTCCCGCCTTCACCCAAACCTCCTACACCCTGTTTCGTC  
CGCGAGAACAACAGCCCCGCCCTGCACATCCGCAGCGTCAGCGCTACAGACAGAGACTCAGG  
CACCAACGCCCAGGTCACCTACTCGCTGCTGCCGCCCCAGGACCCGACCTGCCCCCTCACAT  
CCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTCCGCCCTCAGGTCTCTGGACTACGAG  
GCCCTGCAGGGGTTCCAGTTCCGCGTGGGCGCTTCAGACCACGGCTCCCCGGCGCTGAGCAG  
CGAGGCGCTGGTGCGCGTGGTGGTGGTGGACGCCAACGACAACCTCGCCCTTCGTGCTGTACC  
CGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCCGGGCGGCGGAGCCGGGCTAC  
CTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACGCCTGGCTGTCTACCA  
GCTGCTCAAGGCCACGGAGCTCGGTCTGTTCCGGCGTGTGGGCGCACAAATGGCGAGGTGCGCA  
CCGCCAGGCTGCTGAGCGAGCGCGACGCGGCCAAGCACAGGCTGGTGGTGGTCAAGGAC  
AATGGCGAGCCTCCGCGCTCGGCCACCGCCACGCTGCACGTGCTCCTGGTGGACGGCTTCTC  
CCAGCCCTACCTGCCTCTCCCGGAGGCGGCCCCGACCCAGGCCCAGGCGACTTGCTCACCG  
TCTACCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCTCTTTTCGGTGCTCCTGTTC  
GTGGCGGTGCGGCTGTGTAGGAGGAGCAGGGCGGCCTCGGTGGGTGCTGCTTGGTGCCCGA  
GGGCCCCCTTCCAGGGCATCTTGTGGACATGAGCGGCACCAGGACCCTATCCCAGAGCTACC  
AGTATGAGGTGTGTCTGGCAGGAGGCTCAGGGACCAATGAGTTCAAGTTCCTGAAGCCGATT  
ATCCCCAACTTCCCTCCCCAGTGCCCTGGGAAAGAAATACAAGGAAATTCTACCTTCCCCAA  
TAACTTTGGGTTCAATATTCAAGTACCATAAGTTGACTTTTACATTCCATAGGTATTTTATTT  
TGTGGCATTTCATGCCAATGTTTATTTCCCCCAATTTGTGTGTATGTAATATTGTACGGAT  
TTACTCTTGATTTTTCTCATGTTCTTTCTCCCTTTGTTTTAAAGTGAACATTTACCTTTATT  
CCTGGTTCTT

**FIGURE 163**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314  
<subunit 1 of 1, 798 aa, 1 stop  
<MW: 87552, pI: 4.84, NX(S/T): 5  
MEASGKLICRQRQVLFSFLLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQREFSR  
RGVRVVSARGNKLHLQLNQETADLLLNEKLDREDLCGHTEPCVLRFOVLLLESPFEFFQAELOV  
IDINDHSPVFLDKQMLVKVSESSPPGTTFPLKNAEDLDVGQNNIENYIISPNSYFRVLTRKR  
SDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLDVNDNAPEFEQPFY  
RVQISEDSPVGFLVVKVSATDVDGTGNGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF  
EKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAFEVTMSAFTSPIPENAPETVVALFSVS  
DLDSGENGKISCSIQEDLPFLLKSAENFYTLLTERPLDRESRAEYNITITVTDLGTPMLITQ  
LNMTVLIADVNDNAPAFQTQSYTLFVRENNSPALHIRSVSATDRDSGTNAQVTYSLLPPQDP  
HLPLTSLVSINADNGHLFALRSLDYEALQGFQFRVGASDHGSPALSSEALVRVVVLDANDNS  
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDGSGQNAWLSYQLLKATELGLEFGVWAH  
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHVLLVDGFSQPYLPLPEAAPTQAA  
ADLLTVYLVVALASVSSFLFVSVLLFVAVRLCRRSRAASVGRCLVPEGPLPGHLVDMMSGTRT  
LSQSYQYEVCLAGGSGTNEFKFLKPIIPNFPPQCPGKEIQGNSTFPNNFGFNIQ

**Important features:****Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 685-712

**Cadherins extracellular repeated domain signature.**

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

**ATP/GTP-binding site motif A (P-loop).**

amino acids 285-292

**N-glycosylation site.**

amino acids 418-421, 436-439, 567-570 and 786-789

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**FIGURE 164**

ACCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGCGCGTAGCCGTGC  
GCCGATTGCCTCTCGGCCTGGGCAATGGTCCCGGCTGCCGGTCGACGACCGCCCCGCGTCAT  
GCGGCTCCTCGGCTGGTGGCAAGTATTGCTGTGGGTGCTGGGACTTCCCGTCCGCGGCGTGG  
AGGTTGCAGAGGAAAGTGGTCGCTTATGGTCAGAGGAGCAGCCTGCTCACCTCTCCAGGTG  
GGGGCTGTGTACCTGGGTGAGGAGGAGCTCCTGCATGACCCGATGGGGCCAGGACAGGGCAGC  
AGAAGAGGCCAATGCGGTGCTGGGGCTGGACACCCAAGGCGATCACATGGTGATGCTGTCTG  
TGATTCTTGGGGAAGCTGAGGACAAAGTGAGTTCAGAGCCTAGCGGCGTCACCTGTGGTGCT  
GGAGGAGCGGAGGACTCAAGGTGCAACGTCCGAGAGAGCCTTTTCTCTCTGGATGGCGCTGG  
AGCACACTTCCCTGACAGAGAAGAGGAGTATTACACAGAGCCAGAAGTGGCGGAATCTGACG  
CAGCCCCGACAGAGGACTCCAATAACACTGAAAGTCTGAAATCCCCAAAGGTGAACTGTGAG  
GAGAGAAACATTACAGGATTAGAAAATTTCACTCTGAAAATTTTAAATATGTCACAGGACCT  
TATGGATTTTCTGAACCCAAACGGTAGTGACTGTACTCTAGTCCTGTTTTACACCCCGTGGT  
GCCGCTTTTCTGCCAGTTTGGCCCCTCACTTTAACTCTCTGCCCCGGGCATTTCCAGCTCTT  
CACTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTCTACCAGGTTTGGCACCGTAGC  
TGTTCCCTAATATTTTATTATTTCAAGGAGCTAAACCAATGGCCAGATTTAATCATAACAGATC  
GAACACTGGAAACACTGAAAATCTTCATTTTTTAATCAGACAGGTATAGAAGCCAAGAAGAAT  
GTGGTGGTAACTCAAGCCGACCAAATAGGCCCTCTTCCCAGCACTTTGATAAAAAGTGTGGA  
CTGGTTGCTTGTATTTTCCTTATTCTTTTAAATTAGTTTTATTATGTATGCTACCATTCGAA  
CTGAGAGTATTCGGTGGCTAATTCCAGGACAAGAGCAGGAACATGTGGAGTAGTGATGGTCT  
GAAAGAAGTTGGAAAGAGGAACTTCAATCCTTCGTTTCAGAAATTAGTGCTACAGTTTCATA  
CATTTTCTCCAGTGACGTGTTGACTTGAACTTCAGGCAGATTAAAAGAATCATTTGTTGAA  
CAACTGAATGTATAAAAAAATTATAAACTGGTGTTTTAACTAGTATTGCAATAAGCAAATGC  
AAAAATATTCAATAG

**FIGURE 165**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48333  
><subunit 1 of 1, 360 aa, 1 stop  
><MW: 39885, pI: 4.79, NX(S/T): 7  
MVPAAGRRPPRVMRLLGWWQVLLWVLGLPVRGVEVAEESGRLWSEEQPAHPLQVGAVYLGEE  
ELLHDPMGQDRAAEEANAVLGLDTQGDHVMVLSVIPGEAEDKVSSEPSGVTCGAGGAEDSRC  
NVRESLFSLDGAGAHFPDREEEYYTEPEVAESDAAPTEDSNNTESLKSPKVNCEERNITGLE  
NFTLKILNMSQDLMDFLNPNNGSDCTLVLFYTPWCRFSASLAPHFNSLPRAFPALHFLALDAS  
QHSSLSTRFGTVAVPNILLFQGAKPMAREFNHTDRTLETLETKIFIFNQTGIEAKKNVVVTQADQ  
IGPLPSTLIKSVDWLLVFSLSLFFLISFIMYATIRTESIRWLIPGQEQEHVE

**Important features:****Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 321-340

**Homologous region to dilsufide isomerase**

amino acids 212-302

**N-glycosylation site.**amino acids 165-168, 181-184, 187-190, 194-197, 206-209, 278-281  
and 293-296**Thioredoxin domain**

amino acids 211-227

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**FIGURE 166**

CCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTGCGCGCGCCACGATGCTGCAGGGCCCTGGCT  
CGCTGCTGCTGCTCTTCCTCGCCTCGCACTGCTGCCTGGGCTCGGCGCGCGGGCTCTTCCTC  
TTTGGCCAGCCCGACTTCTCCTACAAGCGCAGCAATTGCAAGCCCATCCCGGTCAACCTGCA  
GCTGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCCAACCTGCTGGGCCACGAGACCA  
TGAAGGAGGTGCTGGAGCAGGCCGGCGCTTGGATCCCGCTGGTCATGAAGCAGTGCCACCCG  
GACACCAAGAAGTTCCTGTGCTCGCTCTTCGCCCCCGTCTGCCTCGATGACCTAGACGAGAC  
CATCCAGCCATGCCACTCGCTCTGCGTGCAGGTGAAGGACCGCTGCGCCCCGGTCATGTCCG  
CCTTCGGCTTCCCCTGGCCCCGACATGCTTGAGTGCGACCGTTTCCCCCAGGACAACGACCTT  
TGCATCCCCCTCGCTAGCAGCGACCACCTCCTGCCAGCCACCGAGGAAGCTCCAAAGGTATG  
TGAAGCCTGCAAAAATAAAAATGATGATGACAACGACATAATGGAAACGCTTTGTAAAAATG  
ATTTTGCACTGAAAATAAAAGTGAAGGAGATAACCTACATCAACCGAGATACCAAATCATC  
CTGGAGACCAAGAGCAAGACCATTTACAAGCTGAACGGTGTGTCCGAAAGGGACCTGAAGAA  
ATCGGTGCTGTGGCTCAAAGACAGCTTGCAGTGCACCTGTGAGGAGATGAACGACATCAACG  
CGCCCTATCTGGTCATGGGACAGAAACAGGGTGGGGAGCTGGTGATCACCTCGGTGAAGCGG  
TGGCAGAAGGGGCAGAGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGCTA  
GTCCCGGCATCCTGATGGCTCCGACAGGCCTGCTCCAGAGCACGGCTGACCATTCTGCTCC  
GGGATCTCAGCTCCCGTTCCCAAGCACACTCCTAGCTGCTCCAGTCTCAGCCTGGGCAGCT  
TCCCCCTGCCTTTTGCACGTTTGCATCCCCAGCATTTCTTGAGTTATAAGGCCACAGGAGTG  
GATAGCTGTTTTACCTAAAGGAAAAGCCACCCGAATCTTGTAGAAATATTCAAATAATA  
AAATCATGAATATTTTAA



**FIGURE 167**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50920

><subunit 1 of 1, 295 aa, 1 stop

><MW: 33518, pI: 7.74, NX(S/T): 0

MLQGPGSLLLLFLASHCCLGSARGLFLFGQPDFSYKRSNCKPIPVNLQLCHGIEYQNMRLPN  
LLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDETIQPCHSLCVQVKDR  
CAPVMSAFGFPPWPDMLECDRFPQDNDLCIPLASSDHLLPATEEAPKVCEACKNKNDDNDIM  
ETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLNGVSEKDLKKSVLWLKDSLQCTCE  
EMNDINAPYLVMGQKQGELVITSVKRWQKGQREFKRISRSIRKLQC

Important features:

Signal peptide:

amino acids 1-20

Cysteine rich domain, homologous to frizzled N terminus

amino acids 6-153

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**FIGURE 168**

GTGGAGGCCGCGACGATGGCGGGGCGGACGGAGGCCGAGACGGGGTTGGCCGAGCCCCGGG  
CCCTGTGCGCGCAGCGGGGCCACCGCACCTACGCGCGCCGCTGGGTGTTCTGCTCGCGATC  
AGCCTGCTCAACTGCTCCAACGCCACGCTGTGGCTCAGCTTTGCACCTGTGGCTGACGTCAT  
TGCTGAGGACTTGGTCCTGTCCATGGAGCAGATCAACTGGCTGTCACTGGTCTACCTCGTG  
TATCCACCCCATTTGGCGTGGCGGCCATCTGGATCCTGGACTCCGTGCGGCTCCGTGCGGCG  
ACCATCCTGGGTGCGTGGCTGAACTTTGCCGGGAGTGTGCTACGCATGGTGCCCTGCATGGT  
TGTTGGGACCCAAAACCCATTTGCCTTCCTCATGGGTGGCCAGAGCCTCTGTGCCCTTGCCC  
AGAGCCTGGTCATCTTCTCTCCAGCCAAGCTGGCTGCCTTGTGGTTCCCAGAGCACCAGCGA  
GCCACGGCCAACATGCTCGCCACCATGTCGAACCCCTCTGGGCGTCCTTGTGGCCAATGTGCT  
GTCCCCCTGTGCTGGTCAAGAAGGGTGAGGACATTCCGTTAATGCTCGGTGTCTATACCATCC  
CTGCTGGCGTCGTCTGCCTGCTGTCCACCATCTGCCTGTGGGAGAGTGTGCCCCCACC  
CCCTCTGCCGGGGCTGCCAGCTCCACCTCAGAGAAGTTCCCTGGATGGGCTCAAGCTGCAGCT  
CATGTGGAACAAGGCCTATGTCATCCTGGCTGTGTGCTTGGGGGGAATGATCGGGATCTCTG  
CCAGCTTCTCAGCCCTCCTGGAGCAGATCCTCTGTGCAAGCGGCCACTCCAGTGGGTTTTCC  
GGCCTCTGTGGCGCTCTCTTCATCACGTTTGGGATCCTGGGGGCACTGGCTCTCGGCCCCCTA  
TGTGGACCGGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGTGCCTGTTCTCTCTGG  
CCTGCGTGCCCTTTGCCCTGGTGTCCCAGCTGCAGGGACAGACCCTTGCCCTGGCTGCCACC  
TGCTCGCTGCTCGGGCTGTTTGGCTTCTCGGTGGGCCCCGTGGCCATGGAGTTGGCGGTCTGA  
GTGTTCCCTTCCCCGTGGGGGAGGGGGCTGCCACAGGCATGATCTTTGTGCTGGGGCAGGCCG  
AGGGAATACTCATCATGCTGGCAATGACGGCACTGACTGTGCGACGCTCGGAGCCGTCTTG  
TCCACCTGCCAGCAGGGGGAGGATCCACTTGACTGGACAGTGTCTCTGCTGCTGATGGCCGG  
CCTGTGCACCTTCTTCAGCTGCATCCTGGCGGTCTTCTTCCACACCCCATACCGGCGCCTGC  
AGGCCGAGTCTGGGGAGCCCCCTCCACCCGTAACGCCGTGGGCGGCGCAGACTCAGGGCCG  
GGTGTGGACCGAGGGGGAGCAGGAAGGGCTGGGGTCCTGGGGCCCAGCACGGCGACTCCGGA  
GTGCACGGCGAGGGGGGCTCGCTAGAGGACCCAGAGGGCCCCGGGAGCCCCCACCAGCCT  
GCCACCGAGCGACTCCCCGTGCGCAAGGCCAGCAGCCACCGACGCGCCCTCCCGCCCCGGC  
AGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTTATTGACCCGGCTGGGTCTCACTCCTCCTT  
CTCCTCCCCGTGGGTGATCACGTAGCTGAGCGCCTTGTAGTCCAGGTTGCCCGCCACATCGA  
TGGAGGCGAACTGGAACATCTGGTCCACCTGCGGGCGGGGGCGAAAGGGCTCCTTGCGGGCT  
CCGGGAGCGAATTACAAGCGCGCACCTGAAAA

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**FIGURE 169**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988  
><subunit 1 of 1, 560 aa, 1 stop  
><MW: 58427, pI: 6.86, NX(S/T): 2  
MAGPTEAETGLAEPRALCAQRGHRTYARRWVFLLAISLLNCSNATLWLSFAPVADVIAEDLV  
LSMEQINWLSLVYLVVSTPFGVAAIWILDSVGLRAATILGAWLNFAGSVLRMVPCMVGTON  
PFAFLMGGQSLCALAQSLVIFSPAKLAALWFPEHORATANMLATMSNPLGVLVANVLSFVLV  
KKGEDIPLMLGVYTIPAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKLQLMWNKA  
YVILAVCLGGMIGISASFSALLEQILCASGHSSGFSGLCGALFITFGILGALALGPYVDRTK  
HFTEATKIGLCLFSLACVPFALVSQLOGQTLALAATCSLLGLEGFSVGPVAMELAVECSFPV  
GEGAATGMIFVLGQAEGILIMLAMTALTVRRSEPSLSTCQQGEDPLDWTVSLLLMAGLCTFF  
SCILAVFFHTPYRRLQAESGEPSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTARG  
ASLEDPRGPGSPHPACHRATPRAQGPAATDAPSRPGRLAGRVQASRFIDPAGSHSSFSSPWVIT

Important features:

Potential Transmembrane domains:

amino acids 30-50, 61-79, 98-112, 126-146, 169-182, 201-215, 248-  
268, 280-300, 318-337, 341-357, 375-387, 420-441

N-glycosylation site.

amino acids 40-43 and 43-46

Glycosaminoglycan attachment site.

amino acids 468-471

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**FIGURE 170A**

GTCCACATCCTGCTCAACTGGGTCAGGTCCTCTTAGACCAGCTCTTGTCATCATTGCT  
GAAGTGGACCAACTAGTTCCCCAGTAGGGGGTCTCCCTGGCAATTCTTGATCGGCGTTGG  
ACATCTCAGATCGCTTCCAATGAAGATGGCCTTGCCTTGGGGTCTGCTTGTTTCATAATCA  
TCTAACTATGGGACAAGGTTGTGCCGGCAGCTCTGGGGGAAGGAGCACGGGGCTGATCAAGC  
CATCCAGGAAACACTGGAGGACTTGTCCAGCCTTGAAAGAAGCTCTAGTGGTTTCTGAATCTA  
GCCCACTTGGCGGTAAGCATGATGCAACTTCTGCAACTTCTGCTGGGGCTTTTGGGGCCAGG  
TGGCTACTTATTTCTTTTAGGGGATTGTGAGGAGGTGACCACTCTCACGGTGAAATACCAAG  
TGTCAGAGGAAGTGCCATCTGGTACAGTGATCGGGAAGCTGTCCAGGAACTGGGCCGGGAG  
GAGAGGCGGAGGCAAGCTGGGGCCGCTTCCAGGTGTTGCAGCTGCCTCAGGCGCTCCCCAT  
TCAGGTGGACTCTGAGGAAGGCTTGCTCAGCACAGGCAGGCGGCTGGATCGAGAGCAGCTGT  
GCCGACAGTGGGATCCCTGCCTGGTTTCTTTGATGTGCTTGCCACAGGGGATTGGCTCTG  
ATCCATGTGGAGATCCAAGTGCTGGACATCAATGACCACCAGCCACGGTTTCCCAAAGGCGA  
GCAGGAGCTGGAAATCTCTGAGAGCGCCTCTCTGCGAACCCTGGATCCCCCTGGACAGAGCTC  
TTGACCCAGACACAGGCCCTAACACCCTGCACACCTACACTCTGTCTCCAGTGAGCACTTT  
GCCTTGGATGTCAATTGTGGGCCCTGATGAGACCAAACATGCAGAACTCATAGTGGTGAAGGA  
GCTGGACAGGGAAATCCATTCAATTTTTTGATCTGGTGTAACTGCCTATGACAATGGGAACC  
CCCCCAAGTCAGGTACCAGCTTGGTCAAGGTCAACGTCTTGGACTCCAATGACAATAGCCCT  
GCGTTTGCTGAGAGTTCACTGGCACTGGAAATCCAAGAAGATGCTGCACCTGGTACGCTTCT  
CATAAACTGACCGCCACAGACCCTGACCAAGGCCCAATGGGGAGGTGGAGTTCTTCCTCA  
GTAAGCACATGCCTCCAGAGGTGCTGGACACCTTCAGTATTGATGCCAAGACAGGCCAGGTC  
ATTCTGCGTCGACCTCTAGACTATGAAAAGAACCCTGCCTACGAGGTGGATGTTTCAGGCAAG  
GGACCTGGGTCCCAATCCTATCCCAGCCCATTGCAAAGTTCTCATCAAGGTCTGGATGTCA  
ATGACAACATCCCAAGCATCCACGTCAATGGGCCTCCCAGCCATCACTGGTGTGAGAAGCT  
CTTCCCAAGGACAGTTTTATTGCTCTTGTCATGGCAGATGACTTGGATTGAGGACACAATGG  
TTTGGTCCACTGCTGGCTGAGCCAAGAGCTGGGCCACTTCAGGCTGAAAAGAAGTAATGGCA  
ACACATACATGTTGCTAACCAATGCCACACTGGACAGAGAGCAGTGGCCCAAATATACCCTC  
ACTCTGTTAGCCCAAGACCAAGGACTCCAGCCCTTATCAGCCAAGAAACAGCTCAGCATTCA  
GATCAGTGACATCAACGACAATGCACCTGTGTTTGAGAAAAGCAGGTATGAAGTCTCCACGC  
GGGAAAACAACCTTACCCTCTCTTCACCTCATTACCATCAAGGCTCATGATGCAGACTTGGGC  
ATTAATGGAAAAGTCTCATACCGCATCCAGGACTCCCCAGTTGCTCACTTAGTAGCTATTGA  
CTCCAACACAGGAGAGGTCACTGCTCAGAGGTCACTGAAGTATGAAGAGATGGCCGGCTTTG  
AGTTCCAGGTGATCGCAGAGGACAGCGGGCAACCCATGCTTGTCATCCAGTGTCTGTGTGG  
GTCAGCCTCTTGATGCCAATGATAATGCCCCAGAGGTGGTCCAGCCTGTGCTCAGCGATGG  
AAAAGCCAGCCTCTCCGTGCTTGTGAATGCCTCCACAGGCCACCTGCTGGTGCCCATCGAGA  
CTCCCAATGGCTTGGGGCCAGCGGGCACTGACACACCTCCACTGGCCACTCACAGCTCCCGG  
CCATTCTTTTGACAACCATTGTGGCAAGAGATGCAGACTCGGGGGCAAATGGAGAGCCCTT  
CTACAGCATCCGCAATGGAAATGAAGCCCACCTCTTCATCCTCAACCCTCATACGGGGCAGC  
TGTTGTCATGTCACCAATGCCAGCAGCCTCATTGGGAGTGAGTGGGAGCTGGAGATAGTA  
GTAGAGGACCAGGGAAGCCCCCTTACAGACCCGAGCCCTGTTGAGGGTCATGTTTGTGAC  
CAGTGTGGACCACCTGAGGGACTCAGCCCGCAAGCCTGGGGCCTTGAGCATGTGATGCTGA  
CGGTGATCTGCCTGGCTGTACTGTTGGGCATCTTCGGGTTGATCCTGGCTTTGTTTCATGTCC  
ATCTGCCGGACAGAAAAGAAGGACAACAGGGCCTACAAGTGTGCGGAGGCGGAGTCCACCTA  
CCGCCAGCAGCCCAAGAGGCCCCAGAAACACATTCAGAAGGCAGACATCCACCTCGTGCCTG  
TGCTCAGGGGTGAGGCAGGTGAGCCTTGTGAAGTCGGGCAGTCCCAAAAGATGTGGACAAG  
GAGGCGATGATGGAAGCAGGCTGGGACCCCTGCCTGCAGGCCCCCTTCCACCTCACCCCGAC  
CCTGTACAGGACGCTGCGTAATCAAGGCAACCAGGGAGCACCGGCGGAGAGCCGAGAGGTGC  
TGCAAGACACGGTCAACCTCCTTTTCAACCATCCAGGCAGAGGAATGCCTCCCGGGAGAAC  
CTGAACCTTCCCGAGCCCCAGCCTGCCACAGGCCAGCCACGTTCCAGGCCTCTGAAGGTGTC  
AGGCAGCCCCACAGGGAGGCTGGCTGGAGACCAGGGCAGTGAGGAAGCCCCACAGAGGCCAC  
CAGCCTCCTCTGCAACCCTGAGACGGCAGCGACATCTCAATGGCAAAGTGTCCCTGAGAAA  
GAATCAGGGCCCCGTGAGATCCTGCGGAGCCTGGTCCGGCTGTCTGTGGCTGCCTTCGCCGA  
GCGGAACCCCGTGGAGGAGCTCACTGTGGATTCTCCTCCTGTTTCAGCAAATCTCCAGCTGC  
TGTCTTGCTGCATCAGGGCCAATCCAGCCCAAACCAACCCAGGAAATAAGTACTTG  
GCCAAGCCAGGAGGCAGCAGGAGTGCAATCCCAGACACAGATGGCCCAAGTGCAAGGGCTGG

**FIGURE 170B**

AGGCCAGACAGACCCAGAACAGGAGGAAGGGCCTTTGGATCCTGAAGAGGACCTCTCTGTGA  
AGCAACTGCTAGAGAAGAAGAGCTGTCAAGTCTGCTGGACCCAGCACAGGTCTGGCCCTGGAC  
CGGCTGAGCGCCCCCTGACCCGGCCTGGATGGCGAGACTCTCTTTGCCCCCTCACCACCAACTA  
CCGTGACAATGTGATCTCCCCGGATGCTGCAGCCACGGAGGAGCCGAGGACCTTCCAGACGT  
TCGGCAAGGCAGAGGCACCAGAGCTGAGCCCAACAGGCACGAGGCTGGCCAGCACCTTTGTC  
TCGGAGATGAGCTCACTGCTGGAGATGCTGCTGGAACAGCGCTCCAGCATGCCCGTGGAGGC  
CGCCTCCGAGGCGCTGCGGCGGCTCTCGGTCTGCGGGGAGGACCCTCAGTTTAGACTTGGCCA  
CCAGTGCAGCCTCAGGCATGAAAGTGCAAGGGGACCCAGGTGGAAAGACGGGGACTGAGGGC  
AAGAGCAGAGGCAGCAGCAGCAGCAGCAGGTGCCTGTGAACATACCTCAGACGCCTCTGGAT  
CCAAGAACCAGGGGCCTGAGGATCTGTGGACAAGAGCTGGTTTCTAAAATCTTGTAACCTCAC  
TAGCTAGCGGCGGCCTGAGAACTTTAGGGTGACTGATGCTACCCCCACAGAGGAGGCAAGAG  
CCCCAGGACTAACAGCTGACTGACCAAAGCAGCCCCCTTGTAAGCAGCTCTGAGTCTTTTGGA  
GGACAGGGACGGTTTGTGGCTGAGATAAGTGTTTCCTGGCAAACATATGTGGAGCACAAAG  
GGTCAGTCCTCTGGCAGAACAGATGCCACGGAGTATCACAGGCAGGAAAGGGTGGCCTTCTT  
GGGTAGCAGGAGTCAGGGGGCTGTACCCTGGGGGTGCCAGGAAATGCTCTCTGACCTATCAA  
TAAAGGAAAAGCAGTAAAAAAAAAAAAAAAAAAAAA



**FIGURE 171**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48331  
<subunit 1 of 1, 1184 aa, 1 stop  
<MW: 129022, pI: 5.20, NX(S/T): 5  
MMQLLQLLLGLLGPGGYLFLLGDCQEVTTTLTVKYQVSEEVPSGTVIGKLSQELGREERRRQA  
GAAFQVLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDPCLVSFDVLATGDLALIHVEIQ  
VLDINDHQPRFPKGEQELEISESASLRTRIPLDRALDPDTGPNTLHTYTLSPSEHFALDVIV  
GPDETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSNDNSPAFAESS  
LALEIQEDAAPGTLLIKLTATDPDQGPNGEVEFFLSKHMPPEVLDTFSIDAKTGQVILRRPL  
DYEKNPAYEVDVQARDLGPNPIPAHCKVLIKVLVDVNDNIPSIHVTWASQPSLVSEALPKDSF  
IALVMADDLDSGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLLAQD  
QGLQPLSAKKQLSIQISDINDNAPVFEKSRYEVSTRENNLPSLHLITIKAHDADLGINGKVS  
YRIQDSPVAHLVAIDSNTGEVTAQRSLNYEEMAGFEFQVIAEDSGQPMLASSVSVVWSLLDA  
NDNAPEVVQPVLSDGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTPLATHSSRPFLTT  
IVARDADSGANGEPLYSIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGS  
PPLQTRALLRVMFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEK  
KDNRAYNCREAESTYRQQPKRPQKHIQKADIHLVPVLRGQAGEPCEVGQSHKDVDKEAMMEA  
GWDPCQLQAPFHLTPTLYRTLNRQGNQGAPAESREVLQDTVNLLFNHPRQRNASRENLNLP  
QPATGQPRSRPLKVAGSPTGRLAGDQGSEEAPQRPPASSATLRRQRHLNGKVSPEKESGPRQ  
ILRSLVRLSVAFAERNPVEELTVDSPPVQQISQLLSLLHQGFQPKPNHRGNKYLAKEP  
RSAIPD TDGPSARAGGQTDPEQEEGPLDPEEDLSVKQLLEEELSSLLDPSTGLALDRLSAPD  
PAWMARLSLPLTTNYRDNVISPDAAATEEPRTFQTFGKAEAPELSPTGTRLASTFVSEMSSL  
LEMLLEQRSSMPVEAASEALRRLSVCGRTLSDLATSAAASGMKVQGDPPGGKTGTGEGKSRGSS  
SSSRCL

**Important features:****Signal peptide:**

amino acids 1-13

**Transmembrane domain:**

amino acids 719-739

**N-glycosylation site.**

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

**Cadherins extracellular repeated domain signature.**

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

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**FIGURE 172**

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGCGAGTCCCGGCTGCAGCACCTGGGAGAAGG  
CAGACCGTGTGAGGGGGCCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAG  
GCAGGAGCCTTCCTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCT  
CCCAGATACTATTTTTTGGATTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTAT  
GAGATACGTCAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTTCTTGCACCAT  
GTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACT  
GGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTTTTCATGGTGCCTTTTACATTGGC  
TATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTTCTGTCTCTT  
ATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTTCCCATTTCTCAGCCCAA  
AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAGTGACTCTC  
ATGGCTCTTCTTTCTGGATTTGGTGTGTCAACTGCCCATACTTACATGTCTTACTTCCT  
CAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATA  
TGATCATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAA  
GTGCATAACAAACCATCAGGTTTCTGGGGAATGATAAAAAGTGTTACCACTTCAGCATCAGG  
AAGTGAAAATCTTACTCTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGC  
TTTTTCTGGAAACAGCTGATCTATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTC  
AAGGGGAAATATTTTAATTTTCTTGGTTACTTTTTCTCTATTTACTGTGTTTGGAAAATTTT  
CATGGCTACCATCAATATTGTTTTTGATCGAGTTGGGAAAACGGATCCTGTCACAAGAGGCA  
TTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTGGTCCCAACACATT  
TCCTTCATTCTTGTTGGAATAATCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTAC  
CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCTCCAATGTCATTGTCCTGCTATTAGCAC  
AGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTTAGAA  
TACCGCACCATTAATCACTGAAGTCCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGTT  
TGATGTGATCTTCCTGGTCAGCGCTCTCTCTAGCATACTCTTCCTCTATTTGGCTCACAAAC  
AGGCACCAGAGAAGCAAATGGCACCTTGAAGTTAAGCCTACTACAGACTGTTAGAGGCCAGT  
GGTTTCAAAATTTAGATATAAGAGGGGGGAAAAATGGAACCAGGGCCTGACATTTTATAAAC  
AAACAAAATGCTATGGTAGCATTTTTCACCTTCATAGCATACTCCTTCCCCGTCAGGTGATA  
CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGGAGAACTAACTCAAGACAATACTCA  
GCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGAGCCAAGAACTAA  
AGGTGAAAAATACACTGGAAGTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGT  
AGGATTTCCGTTTTAAGGTTACATGGAAAAGGTTATAGCTTTGCCTTGAGATTGACTCATT  
AAAATCAGAGACTGTAACAAAAAAGGGGCGGCGGACTCTAGAGTCG  
ACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATG

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**FIGURE 173**

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTEAFSCTMFELIIFEI  
LGVLNSSSRYFHWKMNL CVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTEMYFF  
WKLGDPPF PILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDI  
LALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQ  
QEVDALEELSRQLFLETADLYATKERIEYSKTFKGKYFNFELGYFFSIYCVWKIFMATINIVF  
DRVGKTDPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKEFFYAIS  
SKSSNVIVLLLAQIMGYFVSSVLLIRMSMPLEYRTIITEVLGELQNFYHRWFDVIFLVSA  
LSSILFLYLAHKQAPEKQMAP

**Important features:****Signal peptide:**

amino acids 1-23

**Potential transmembrane domains:**amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444**N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

**Eukaryotic cobalamin-binding proteins**

amino acids 151-160

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**FIGURE 174**

CATGGGAAGTGGAGCCGGAGCCTTCCTTACACTCGCCATGAGTTTCCTCATCGACTCCAGCA  
TCATGATTACCTCCCNGANACTATTTTTTGGATTGGGTGGCTTTTCTTCNGCGCCAATGTT  
TAAAGACTATGAGATACGTCAGTATGTTGTACNGGTGATCTTCTCCGTGACGTTTGCCATTT  
CTTGCACCATGTTTGAGCTCATCATCTTTGAAATCTTNGGAGTATTGAATAGCAGCTCCCGT  
TATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTNTCATGGTGCCTTT  
TTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTT  
CCTGTCTCTTATGGCTGACCTTTATGTATTTCCAG

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**FIGURE 175**

GTGTTGCCCTTGGGGAGGGGAAGGGGAGCCNGGCCCTTTCCTAAAATTTGGCCAAGGGTTTC  
TTTNTTGAATTCCGGGTTNNGNATACCTTCCCAGAAAATATTTTTTGGATTGGGGTAGNTT  
TTTTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATNTT  
NTCCGTGACGTTTGCATTTTCTTGCACCATGTTTGAGCTCATCATNTTTGAAATNTTAGGAG  
TATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATC  
CTGGTTTTTCATGGTGCCTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA  
TAAACAACGACTGCTTTTTTCTGTCTNTTATGGCTGACCTTTATGTATTTNTTNTGGAAAN  
TAGGAGATCCCTTTCCCATTC

**FIGURE 176A**

CTCGCGCAGGGATCGTCCCATGGCCGGGGCTCGGAGCCGCGACCCTTGGGGGGCCTCCGGGA  
TTTGCTACCTTTTTTGGCTCCCTGCTCGTCGAACCTGCTCTTCTCACGGGCTGTGCGCTTCAAT  
CTGGACGTGATGGGTGCCTTGCGCAAGGAGGGGCGAGCCAGGCAGCCTCTTCGGCTTCTCTGT  
GGCCCTGCACCGGCAGTTGCAGCCCCGACCCCAGAGCTGGCTGCTGGTGGGTGCTCCCCAGG  
CCCTGGCTCTTCTTGGGCAGCAGGCGAATCGCACTGGAGGCCTCTTCGCTTGCCCGTTGAGC  
CTGGAGGAGACTGACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAAGGAAAG  
CAAGGAGAACCAGTGGTTGGGAGTCAGTGTTCGGAGCCAGGGGGCCTGGGGGCAAGATTGTTA  
CCTGTGCACACCGATATGAGGCAAGGCAGCGAGTGGACCAGATCCTGGAGACGCGGGATATG  
ATTGGTCGCTGCTTTGTGCTCAGCCAGGACCTGGCCATCCGGGATGAGTTGGATGGTGGGGA  
ATGGAAGTTCTGTGAGGGACGCCCCCAAGGCCATGAACAATTTGGGTCTGCCAGCAGGGCA  
CAGCTGCCGCCCTTCTCCCCTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAACCTATAAT  
TGGAAGGGCACGGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGACCTGGCACACCTGGA  
CGACGGTCCCTACGAGGCGGGGGGAGAGAAGGAGCAGGACCCCCGCTCATCCCGGTCCCTG  
CCAACAGCTACTTTGGCTTCTCTATTGACTCGGGGAAAGGTCTGGTGGTGCAGAAGAGCTG  
AGCTTTGTGGCTGGAGCCCCCGCGCCAACCACAAGGGTGTGTGGTCATCCTGCGCAAGGA  
CAGCGCCAGTCGCCTGGTGGCCGAGGTTATGCTGTCTGGGGAGCGCCTGACCTCCGGCTTTG  
GCTACTCACTGGCTGTGGCTGACCTCAACAGTGATGGCTGGCCAGACCTGATAGTGGGTGCC  
CCCTACTTCTTTGAGCGCCAAGAAGAGCTGGGGGGTGTGTGTATGTGTACTTGAACCAGGG  
GGGTCACTGGGCTGGGATCTCCCCTCTCCGGCTCTGCGGCTCCCCTGACTCCATGTTCCGGA  
TCAGCCTGGCTGTCTGGGGGACCTCAACCAAGATGGCTTTCCAGATATTGCAGTGGGTGCC  
CCCTTTGATGGTGTATGGGAAAGTCTTCATCTACCATGGGAGCAGCCTGGGGGTGTGCGCAA  
ACCTTCACAGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGAGCTTCGGCTACTCCCTGTCAG  
GCAGCTTGATATGGATGGGAACCAATACCTGACCTGCTGGTGGGCTCCCTGGCTGACACC  
GCAGTGCTCTTCAGGGCCAGACCCATCCTCCATGTCTCCCATGAGGTCTCTATTGCTCCACG  
AAGCATCGACCTGGAGCAGCCCAACTGTGCTGGCGGCCACTCGGTCTGTGTGGACCTAAGGG  
TCTGTTTTCAGCTACATTGCAGTCCCCAGCAGCTATAGCCCTACTGTGGCCCTGGACTATGTG  
TTAGATGCGGACACAGACCGGAGGCTCCGGGGCCAGGTTCCCCGTGTGACGTTCTTGAGCCG  
TAACCTGGAAGAACCCAAGCACCAGGCCTCGGGCACCGTGTGGCTGAAGCACCAGCATGACC  
GAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAAATGTCAAAGACAAGCTTCGGGCCATT  
GTAGTGACCTTGTCTACAGTCTCCAGACCCCTCGGCTCCGGCGACAGGCTCCTGGCCAGGG  
GCTGCCTCCAGTGGCCCCCATCCTCAATGCCACCAGCCCAGCACCAGCGGGCAGAGATCC  
ACTTCCTGAAGCAAGGCTGTGGTGAAGACAAGATCTGCCAGAGCAATCTGCAGCTGGTCCAC  
GCCCCGCTTCTGTACCCGGGTGAGCGACACGGAATTCCAACCTCTGCCCATGGATGTGGATGG  
AACAACAGCCCTGTTTGCAGTGAAGTGGGCAGCCAGTCATTGGCCTGGAGCTGATGGTCACCA  
ACCTGCCATCGGACCCAGCCCAGCCCCAGGCTGATGGGGATGATGCCCATGAAGCCCAGCTC  
CTGGTCATGCTTCTTCACTCACTGCACTACTCAGGGGTCCGGGGCCCTGGACCTGCGGAGAA  
GCCACTCTGCCTGTCCAATGAGAATGCCTCCCATGTTGAGTGTGAGCTGGGGAAACCCCATGA  
AGAGAGGTGCCAGGTCACCTTCTACCTCATCCTTAGCACCTCCGGGATCAGCATTGAGACC  
ACGGAACTGGAGGTAGAGCTGCTGTTGGCCACGATCAGTGAGCAGGAGCTGCATCCAGTCTC  
TGCACGAGCCCCGTGTCTTCAATTGAGCTGCCACTGTCCATTGCAGGAATGGCCATTCCCCAGC  
AACTCTTCTTCTCTGGTGTGGTGAAGGGGCGAGAGAGCCATGCAGTCTGAGCGGGATGTGGGC  
AGCAAGGTCAAGTATGAGGTACGGTTCCTCAACCAAGGCCAGTCGCTCAGAACCCTGGGCTC  
TGCCTTCTCAACATCATGTGGCCTCATGAGATTGCCAATGGGAAGTGGTTGCTGTACCCAA  
TGCAGGTTGAGCTGGAGGGCGGGCAGGGGCCCTGGGCAGAAAGGGCTTTGCTCTCCAGGCCC  
AACATCCTCCACCTGGATGTGGACAGTAGGGATAGGAGGCGGGGAGCTGGAGCCACCTGA  
GCAGCAGGAGCCTGGTGAAGCGGCAGGAGCCCAGCATGTCTTGGTGGCCAGTGTCTCTGCTG  
AGAAGAAGAAAAACATCACCTGGACTGCGCCCCGGGGCACGGCCAACCTGTGTGGTGTTCAGC  
TGCCCACTCTACAGCTTTGACCGCGCGGCTGTGCTGCATGTCTGGGGCCGTCTCTGGAACAG  
CACCTTTCTGGAGGAGTACTCAGCTGTGAAGTCCCTGGAAGTGATTGTCCGGGCCAACATCA  
CAGTGAAGTCTCCATAAAGAACTTGATGCTCCGAGATGCCTCCACAGTGATCCAGTGATG  
GTATACTTGGACCCCATGGCTGTGGTGGCAGAAGGAGTGCCCTGGTGGGTGATCCTCCTGGC  
TGTACTGGCTGGGCTGCTGGTGTAGCACTGCTGGTGTGCTCCTGTGGAAGATGGGATTCT  
TCAAACGGGCGAAGCACCCCGAGGGCCACCGTGCCCCAGTACCATGCGGTGAAGATTCTCGG  
GAAGACCGACAGCAGTTCAAGGAGGAGAAGACGGGCACCATCCTGAGGAACAACCTGGGGCAG

**FIGURE 176B**

CCCCCGGCGGGAGGGCCCGGATGCACACCCCATCCTGGCTGCTGACGGGCATCCCGAGCTGG  
GCCCCGATGGGCATCCAGGGCCAGGCACCGCCCTAGGTTCCCATGTCCCAGCCTGGCCTGTGG  
CTGCCCTCCATCCCTTCCCCAGAGATGGCTCCTTGGGATGAAGAGGGTAGAGTGGGCTGCTG  
GTGTCGCATCAAGATTTGGCAGGATCGGCTTCCTCAGGGGCACAGACCTCTCCCACCCACAA  
GAACTCCTCCCACCCAACTTCCCCTTAGAGTGCTGTGAGATGAGAGTGGGTAAATCAGGGAC  
AGGGCCATGGGGTAGGGTGAGAAGGGCAGGGGTGTCCTGATGCAAAGGTGGGGAGAAGGGAT  
CCTAATCCCTTCCTCTCCCATTCACCCTGTGTAAACAGGACCCCAAGGACCTGCCTCCCCGGA  
AGTGCCTTAACCTAGAGGGTCGGGGAGGAGGTTGTGTCACTGACTCAGGCTGCTCCTTCTCT  
AGTTTCCCCTCTCATCTGACCTTAGTTTGCTGCCATCAGTCTAGTGGTTTCGTGGTTTCGTC  
TATTTATTAAAAATATTTGAGAACAAAAAAAAAAAAAAAAAAAAA

**FIGURE 177**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL  
QPRPQSWLLVGAPQALALPGQQANRTGGLFACPLSLEETDCYRVDIDQADMOKESKENQWL  
GVSVRSQGPGGKIVTCAHRYEARQRVDQILETRDMIGRCFVLSQDLAIRDELDDGGGEWKFC  
RPOGHEQFGFCQOGTAAAFSPDSHYLLFGAPGTYNWKGRTARVELCAQGSADLAHLDDGPYEA  
GGEKEQDPRLIPVPANSYFGFSIDSGKGLVRAEELS FVAGAPRANHKGAVVILRKDSASRLV  
PEVMLSGERLTSGFGYSLAVADLNSDGWPDLLVIGAPYFFERQEELGGAVYVYLNQGGHWAGI  
SPLRLCGSPDSMFGISLAVLGDLNQGDFDIAVGAPFDGDGKVFIYHGSSLGVVAKPSQVLE  
GEAVGIKSGYSLSGSLDMDGNQYPDLLVGSGLADTAVLFRARPILHVSHEVSIAPRSIDLEQ  
PNCAGGHSVCVDLRVCFSYIAVPSSYSPTVALDYVLDADTDRLRGQVPRVTFLSRNLEEPK  
HQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSSYSLQTPRLRRQAPGQGLPPVAP  
ILNAHQPSTQRAEIHFLKQCGCEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVDGTTALFA  
LSGQPVIGLELMVTNLPSDPAQPDAGDDAHEAQLLVMLPDSLHYSQVRLDPAEKPLCLSN  
ENASHVECELGNPMKRGAQVTFFYLILSTSGIS IETTELEVELLATISEQELHPVSARARVF  
IELPLS IAGMAIPQQLFFSGVVRGERAMQSERDVGSKVKYEVTVSNQGQSLRTLGS AFLNIM  
WPHEIANGKWLLYPMQVELEGGQGPQKGLCSRPNIHLVDVDSRDRRRRELEPPEQQEPGE  
RQEPSMSWVPVSSAEKKKNITLDCARGTANCVVFSCPLYSFDRAAVLHVWGRLWNSTFLEFY  
SAVKSLEVIVRANITVKSSIKNMLRDASTVIPVMVYLDPMVVAEGVPWWVILLAVLAGLL  
VLALLVLLLWKMGFFKRAKHPEATVPQYHAVKIPREDRQQFKEEKTGTILRNNWGS PRREGP  
DAHPILAADGHPGLGPDGHPGPGTA

**Important features:****Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 1039-1064

**N-glycosylation sites.**

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

**Integrins alpha chain proteins.**

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

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**FIGURE 178**

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGCGTGCAGCAGCTCCAGA  
AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCT  
CACAAACAAGATGCTCAAGGTGTCAGCCGTAAGTGTGTGTGTGTGCAGCCGCTTGGTGCAGTCA  
GTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGGGGCGGTCCGACGGCGGTAATTTTC  
TGGATGATAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAC  
AAATTCCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAACCCTTCGA  
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTAT  
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATG  
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATAATTATCCACCTGCAAGCAGTG  
CCCAGTGGTCTATCCCAGCCCTGTTTGTGGTTCAGATGGTCATACCTACTCTTTTCAGTGCA  
AACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGGACATTGC  
CCATGTCCTTCAGATAAGCCCACCAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCT  
GGAGTTCAGGGAAGTGGCAAACAGATTGCGGGACTGGTTCAGGCCCTTCATGAAAGTGGAA  
GTCAAAACAAGAAGACAAAAACATTGCTGAGGCCTGAGAGAAGCAGATTGATACCAGCATC  
TTGCCAATTTGCAAGGACTCACTTGGCTGGATGTTTAACAGACTTGATACAACTATGACCT  
GCTATTGGACCAGTCAGAGCTCAGAAGCATTACCTTGATAAGAATGAACAGTGTACCAAGG  
CATTCTTCAATTCTTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTGCTAC  
TGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCA  
AGGGGTAAAGAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGC  
CAACACAATGTCATGGCAGTGTGGACAGTGCTGGTGTGTTGACAGATATGGAAATGAAGTC  
ATGGGATCCAGAATAAATGGTGTTCAGATTGTGCTATAGATTTTGAGATCTCCGGAGATTT  
TGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATG  
ATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGATGAC  
CATGATGTATACATTTGATTGATGACAGTTGAAATCAATAAATCTACATTTCTAATATTTA  
CAAAAATGATAGCCTATTTAAAATTATCTTCTTCCCCAATAACAAAATGATTCTAAACCTCA  
CATATATTTTGTATAATTATTTGAAAAATTGCAGCTAAAGTTATAGAACTTTATGTTTAAAT  
AAGAATCATTTGCTTTGAGTTTTTATATTCTTACACAAAAGAAAATACATATGCAGTCTA  
GTCAGACAAAATAAAGTTTTGAAGTGCTACTATAATAAATTTTTCACGAGAACAACTTTGT  
AAATCTTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTGAAG  
ATAATTCTAAGTGAAATTTAAAATAAATAAATTTTTAATGACCTGGGTCTTAAGGATTTAGG  
AAAAATATGCATGCTTTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG  
GATAACAGAGAGATACCACATGACTCCAAAAA



**FIGURE 179**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829  
><subunit 1 of 1, 436 aa, 1 stop  
><MW: 49429, pI: 4.80, NX(S/T): 0  
MLKVSAVLCVCAAAWCSQSLAAAAVAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFR  
DEVEDDYFRTWSPGKPFQALDPAKDPCLKMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEA  
GVDHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCP  
SDKPTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKKTLLRPERSRFDTSILPI  
CKDSLGMFNRLLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQ  
RQODPPCQTELSNIQKRQGVKKLLGQYIPLCDEDGYKPTQCHGSGVQCWCVD RYGNV MGS  
RINGVADCAIDFEISGDFASGDFHEWTDDEDEDDIMNDEDEIEDDDEDEGGDDDDGGDDHVDVYI

**Important features:**

**Signal peptide:**

amino acids 1-16

**Leucine zipper pattern.**

amino acids 246-267

**N-myristoylation sites.**

amino acids 357-362, 371-376 and 376-381

**Thyroglobulin type-1 repeat proteins**

amino acids 353-365 and 339-352

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**FIGURE 180A**

CAGACTCCAGATTTCCCTGTCAACCACGAGGAGTCCAGAGAGGAAACGCGGAGCGGAGACAA  
CAGTACCTGACGCCTCTTTCAGCCCCGGGATCGCCCCAGCAGGGATGGGCGACAAGATCTGGC  
TGCCCTTCCCCGTGCTCCTTCTGGCCGCTCTGCCTCCGGTGCTGCTGCCTGGGGCGGCCGGC  
TTCACACCTTCCCTCGATAGCGACTTCACCTTTACCCTTCCCGCCGGCCAGAAGGAGTGCTT  
CTACCAGCCCATGCCCCCTGAAGGCCTCGCTGGAGATCGAGTACCAAGTTTTAGATGGAGCAG  
GATTAGATATTGATTTCCATCTTGCCTCTCCAGAAGGCCAAAACCTTAGTTTTTGAACAAAGA  
AAATCAGATGGAGTTCACACTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACAA  
TACATTGAGCACCATTCTGAGAAGGTGATTTTCTTTGAATTAATCCTGGATAATATGGGAG  
AACAGGCACAAGAACAAGAAGATTGGAAGAAATATATTACTGGCACAGATATATTGGATATG  
AAACTGGAAGACATCCTGGAATCCATCAACAGCATCAAGTCCAGACTAAGCAAAAGTGGGCA  
CATACAAATTCTGCTTAGAGCATTGGAAGCTCGTGATCGAAACATACAAGAAAGCAACTTTG  
ATAGAGTCAATTTCTGGTCTATGGTTAATTTAGTGGTCATGGTGGTGGTGTGAGCCATTCAA  
GTTTATATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAAGTAGAACTTAAACTCCAACT  
AGAGTACGTAACATTGAAAAATGAGGCATAAAAATGCAATAAACTGTTACAGTCAAGACCAT  
TAATGGTCTTCTCCAAAATATTTTGAGATATAAAAGTAGGAAACAGGTATAATTTTAATGTG  
AAAATTAAGTCTTCACTTTCTGTGCAAGTAATCCTGCTGATCCAGTTGTACTTAAGTGTGTA  
ACAGGAATATTTTGCAGAATATAGGTTTAACTGAATGAAGCCATATTAATAACTGCATTTTC  
CTAACTTTGAAAAATTTTGCAAATGTCTTAGGTGATTTAAATAAATGAGTATTGGGCCATAAT  
TGCAACACCAGTCTGTTTTTAACAGGTTCTATTACCCAGAAGCTTTTTTGTAAATGCGGCAGT  
TACAAATTAAGTGTGGAAGTTTTCAAGTTTTAAGTTATAAATCACCTGAGAATTACCTAATGA  
TGGATTGAATAAATCTTTAGACTACAAAAGCCCAACTTTTTCTCTATTACATATGCATCTCT  
CCTATAATGTAAATAGAATAATAGCTTTGAAATACAATTAGGTTTTTGAGATTTTTTATAACC  
AAATACATTTTCAAGTGTAAATATAGCAGAAAGCATTAGTCTTTGTACTTTGCTTACATTCC  
CAAAGCTGACATTTTCAAGATTCTTAAACACAAAGTTACACTTACTAAAATTAGGACAT  
GTTTTCTCTTTGAAATGAAGAATATAGTTTAAAGCTTCTCCTCCATAGGGACACATTTTC  
TCTAACCTTAACTAAAGTGTAGGATTTTAAATTAATGTGAGGTAAAATAAGTTTTATTTT  
TAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAATAATCATGTTATGTTAATTTTAAC  
ATGATTGCTGACTTGGATAATTCATTATTACCAGCAGTTATGAAGGAAATATTGCTAAAATG  
ATCTGGGCCTACCATAAATAAATATCTCCTTTTCTGAGCTCTAAGAATTATCAGAAAACAGG  
AAAGAATTTAGAAAACTTGAGAAAACCTAATCCAAAATAAATTCACTTAAGTAGAACTAT  
AAATAAATATCTAGAATCTGACTGGCTCATCATGACATCCTACTCATAACATAAATCAAAGG  
AGATGATTAATTTCCAGTTAGCTGGAAGAACTTTGGCTGTAGGTTTTTATTTTCTACAAGA  
ATTCTGGTTTGAATTATTTTGTAGCAGGTACATTTTATAAAATGTAAGCCCTACTGTAAG  
GTTTAGCACTGGGTGTACATATTTATTAAAAATTTTATTATAAACAATTTTATTAAAAATGG  
CCTTTCTGAACACTTTATTTATTGATGTTGAAGTAAGGATTAGAAACATAGACTCCCAAGTT  
TTAAACACCTAAATGTGAATAACCCATATATACAACAAAGTTTCTGCCATCTAGCTTTTTGA  
AGTCTATGGGGGTCTTACTCAAGTACTAGTAATTTAACTTCATCATGAATGAAGTATAATTT  
TTAAGTTATGCCCATTATAACGTTGTTTATGACTACATTGTGAGTTAGAAACAACTTAAA  
ATTTGGGGTATAGAACCCTCAACAGGTTAGTAATGCTGGAATTCCTGATGAGCAATAATGA  
TAACCAGAGAGTGATTTTCACTTACACTCATAGTAGTATAAAAAGAGATACATTTCCCTCTTA  
GGCCCTGGGAGAAGAGCAGCTTAGATTTCCCTACTGGCAAGGTTTTTAAAAATGAGGTAAA  
TGCCGTATATGATCAATTACCTTAATTGGCCAAGAAAATGCTTCAGGTGTCTAGGGGTATCC  
TCTGCAACACTTGCAAGACAAAGGTCAATAAGATCCTTGCCATGAATACCCCTCCCTTTTG  
CGCTGTTAAATTTGCAATGAGAAGCAAATTTACAGTACCATAACTAATAAAGCAGGGTACAG  
ATATAAACTACTGCATCTTTTCTATAAACTGTGATTAAGAATTCTACCTCTCCTGTATGGC  
TGTTACTGTACTGTACTCTGACTCCTTACCTAACAATGAATTTGTTACATAATCTTCTAC  
ATGTATGATTTGTGCCACTGATCTTAAACCTATGATTTCAGTAACTTCTTACCATATAAAAAC  
GATAATTGCTTTATTTGGAAAAGAATTTAGGAATACTAAGGACAATTATTTTATAGACAAA  
GTAAAAAGACAGATATTTAAGAGGCATAACCAAAAAGCAAACTTGTAACAGAGTAAAAA  
TCTTTAATATTTCTAAAGACATACTGTTTATCTGCTTCATATGCTTTTTTTAATTTCACTAT  
TCCATTTCTAAATTAAAGTTATGCTAAATTGAGTAAGCTGTTTATCACTTAACAGCTCATTT  
TGTCTTTTTCAATATACAAATTTTAAAAATACTACAATATTTAACTAAGGCCCAACCGATTT  
CCATAATGTAGCAGTTACCGTGTTCACCTCACACTAAGGCCTAGAGTTTGCTCTGATATGCA  
TTTGGATGATTAATGTTATGCTGTTCTTTCATGTGAATGTCAAGACATGGAGGGTGTGTTGTA

**FIGURE 180B**

ATTTTATGGTAAAATTAATCCTTCTTACACATAATGGTGTCTTAAAATTGACAAAAATGAG  
CACTTACAATTGTATGTCTCCTCAAATGAAGATTCTTTATGTGAAATTTTAAAAGACATTGA  
TTCCGCATGTAAGGATTTTTCATCTGAAGTACAATAATGCACAATCAGTGTTGCTCAAACCTG  
CTTTATACTTATAAACAGCCATCTTAAATAAGCAACGTATTGTGAGTACTGATATGTATATA  
ATAAAAATTATCAAAGGAAAA

**FIGURE 181**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196  
><subunit 1 of 1, 229 aa, 1 stop  
><MW: 26017, pI: 4.73, NX(S/T): 0  
MGDKIWLPFPVLLLAALPPVLLPGAAGFTPSLSDFTFTLPAGQKECFYQPMPLKASLEIEY  
QVLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFSTISEKVIFTEL  
ILDNMGEQAQEQEDWKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRN  
IQESNFDRLVNFWSMVNLVVMVVSAIQVYMLKSLFEDKRKSRT

**Important features:****Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 195-217

**N-myristoylation site.**

amino acids 43-48

**Tyrosine kinase phosphorylation site.**

amino acids 55-62

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**FIGURE 182**

CCATCCCTGAGATCTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGAT  
CTCACCAGAGAGTCGCAGACACTATGCTGCCTCCCATGGCCCTGCCAGTGTGTCCTGGATG  
CTGCTTTCCTGCCTCATTCTCCTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAACTGCC  
CTCTCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGT  
TTTTGTCACCAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAA  
CTGGTGTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCCTCCCTGGTGAGGAGCATTAG  
TAACAGCTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATG  
GAGATGGATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCC  
TCCACCATCTTAAACCCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTG  
GAAAGATTATAACTGTGATGCAAAGTTACCCTATGTCTGCAAGTTCAAGGACTAGGGCAGGT  
GGGAAGTCAGCAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGAC  
TCACCCTGGAAGAGAATATTCTCCCCAACTGCCCTACCTGACTACCTTGTCATGATCCTCC  
TTCTTTTTCCTTTTTCTTCACCTTCATTCAGGCTTTTCTCTGTCTTCCATGTCTTGAGATC  
TCAGAGAATAATAATAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 183**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965

<subunit 1 of 1, 175 aa, 1 stop

<MW: 19330, pI: 7.25, NX(S/T): 1

MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM  
DADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSS  
TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

Important features:

Signal peptide:

amino acids 1-26

C-type lectin domain signature.

amino acids 146-171

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**FIGURE 184**

CCAGTCTGTCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC  
ACAGAGGAGTGGGCCGGGACCATGCGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGCTGGC  
TGCCTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCCACAGGAGTGT  
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC  
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA  
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCGTGTCTGCTGCAATACTG  
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGCCCTCACGCTC  
CTCCCACCTCTTGAGCCTCCGACTGTAGAGTCCCCGCCACCCCCATGGCCCTATGCGGCCCA  
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAAAAA



**FIGURE 185**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP  
FQGDSTVTKSCASKCKPSDVDGIGQTLVPSCCNTELCNVDGAPALNSLHCGALTLLPLLSRL

Important features:

Signal peptide:

amino acids 1-17

N-glycosylation site.

amino acids 46-49

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**FIGURE 186**

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGC  
ACGGTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTTCTCCCTCTT  
GAGTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGGATGG  
TAGCGGCGGCTCTCGGCGGCCACCCTCTGCTGGGAGTGAGCGCCACCTTGAACCTCGGTTCTC  
AATTCCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTC  
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA  
ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACCTGATGAGTACTGCGCTAGT  
CCCACCCGCGGAGGGGACGCGAGGCGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACG  
CTGCATGCGTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTT  
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT  
CATAGCACCTTGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAA  
AGGACAAGAAGGTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTA  
GACACTTCTGGTCCAAGATCTGTAAACCTGTCCTGAAAGAAGGTCAAGTGTGTACCAAGCAT  
AGGAGAAAAGGCTCTCATGGACTAGAAATATTCAGCGTTGTTACTGTGGAGAAGGTCTGTC  
TTGCCGGATACAGAAAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTCAGA  
GACACTAAACCAGCTATCCAAATGCAGTGAACCTCTTTTATATAATAGATGCTATGAAAACC  
TTTTATGACCTTCATCAACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCAT  
TCCAATAACACCTTCCAAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACTCCCCTG  
TGATTGCAGTAAATTACTGTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGA  
AACTTTTAATTATTTTTCTAAAGGTGCTGCACTGCCTATTTTTCTCTTGTATGTAAATTT  
TTGTACACATTGATTGTTATCTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATT  
TCAGCTTATAGTTCTTAAAAGCATAACCCCTTACCCCATTTAATTCTAGAGTCTAGAACGCA  
AGGATCTCTTGGAATGACAAATGATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATT  
TTCTGAAATGTACTATCTTAATGCTTAAATTATTTCCCTTTAGGCTGTGATAGTTTTTGA  
AATAAAATTTAACATTTAAAAA

**FIGURE 187**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57530

<subunit 1 of 1, 266 aa, 1 stop

<MW: 28672, pI: 8.85, NX(S/T): 1

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA  
APGILYPGGNKYQOTIDNYQPYPCAEDDEECGTDEYCASPTRGGDAGVQICLACRKRRKRCMRH  
AMCCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEG  
SVCLRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHRRKGSHGLEIFQRCYCGEGLSCRIQ  
KDHHQASNSSRLHTCQRH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 256-259

Fungal Zn(2)-Cys(6) binuclear cluster domain

amino acids 110-126

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**FIGURE 188**

TGTGTTTCCCTGCAGTCAGAATTTGGGACNGCAGGGGTTCCCGGACCTGATTTTGCAGCGGA  
ACGGGAAGGTTTTGTGGGACCCAGGTTGAAATGACGETCATTTTTTTTTCTTTCTCCTTCNG  
GAGTCCTTNTGAGANGATGGTTTTGGGCGCAGCGGGAGCTAACCCGGTTTTTTGTNGCGATG  
GTAGCGGCGGTTTTTCGGCGGGCCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTTC  
AATTCCAACGNTATCAAGAACCTGCCCCCACCNTGGGCGGCGCTGCGGGGCACCCAGGNTT  
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA  
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT  
CCCACCCGCGGAGGGGGANGCGGGCGTGCAAATNTGTNTNGCCTGCAGGAAGCGCCGAAAACG  
CTGCATGCGTCANGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTNTT  
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT  
CATAGCACCTTGGATGGG

**FIGURE 189A**

GAGGAACCTACCGGTACCGGCCGCGCGCTGGTAGTCGCCGGTGTGGCTGCACCTCACCAATC  
CCGTGCGCCGCGGCTGGGCCGTCCGAGAGTGCGTGTGCTTCTCTCCTGCACGCGGTGCTTGG  
GCTCGGCCAGGCGGGGTCCGCCGCCAGGGTTTGAGGATGGGGGAGTAGCTACAGGAAGCGAC  
CCCGCGATGGCAAGGTATATTTTTGTGGAATGAAAAGGAAGTATTAGAAATGAGCTGAAGAC  
CATTCACAGATTAATATTTTTGGGGACAGATTTGTGATGCTTGATTCACCCCTGAAGTAATG  
TAGACAGAAGTTCTCAAATTTGCATATTACATCAACTGGAACCAGCAGTGAATCTTAATGTT  
CACTTAAATCAGAACTTGCAATAAGAAAGAGAATGGGAGTCTGGTTAAATAAAGATGACTATA  
TCAGAGACTTGAAAAGGATCATTCTCTGTTTTCTGATAGTGTATATGGCCATTTTAGTGGGC  
ACAGATCAGGATTTTACAGTTTACTTGGAGTGTCCAAACTGCAAGCAGTAGAGAAATAAG  
ACAAGCTTTCAAGAAATTGGCATTGAAGTTACATCCTGATAAAAACCCGAATAACCCAAATG  
CACATGGCGATTTTTTAAATAAATAGAGCATATGAAGTACTCAAAGATGAAGATCTACGG  
AAAAAGTATGACAAATATGGAGAAAAGGGACTTGAGGATAATCAAGGTGGCCAGTATGAAAG  
CTGGAACATATTATCGTTATGATTTTGGTATTTATGATGATGATCCTGAAATCATAACATTGG  
AAAGAAGAGAATTTGATGCTGCTGTTAATTCTGGAGAACTGTGGTTTGTAATTTTTACTCC  
CCAGGCTGTTTCACTGCCATGATTTAGCTCCACATGGAGAGACTTTGCTAAAGAAGTGGA  
TGGGTTACTTCGAATTGGAGCTGTTAACTGTGGTGATGATAGAATGCTTTGCCGAATGAAAG  
GAGTCAACAGCTATCCAGTCTCTTCATTTTTTCGGTCTGGAATGGCCCCAGTGAAATATCAT  
GGAGACAGATCAAAGGAGAGTTTAGTGAGTTTTGCAATGCAGCATGTTAGAAGTACAGTGAC  
AGAACTTTGGACAGGAAATTTGTCAACTCCATACAACTGCTTTTGCTGCTGGTATTGGCT  
GGCTGATCACTTTTTGTTCAAAGGAGGAGATTGTTTGACTTCACAGACACGACTCAGGCTT  
AGTGGCATGTTGTTTCTCAACTCATTGGATGCTAAAGAAATATATTTGGAAGTAATACATAA  
TCTTCCAGATTTTGAACACTTTTCGGCAAACACACTAGAGGATCGTTTGCTCATCATCGGT  
GGCTGTTATTTTTTTCATTTTGGAAAAAATGAAAATTCAAATGATCCTGAGCTGAAAAAACTA  
AAAACCTCTACTTAAAAATGATCATATTCAAGTTGGCAGGTTTGACTGTTCTCTGCACCAGA  
CATCTGTAGTAATCTGTATGTTTTTCAGCCGTCTCTAGCAGTATTTAAAGGACAAGGAACCA  
AAGAATATGAAATTCATCATGGAAAGAAGATTCTATATGATATACTTGCCCTTGCCAAAGAA  
AGTGTGAATTCTCATGTTACCACGCTTGACCTCAAATTTTCTGCCAATGACAAAGAACC  
ATGGCTTGTTGATTTCTTTGCCCCCTGGTGTCCACCATGTCGAGCTTTACTACCAGAGTTAC  
GAAGAGCATCAAATCTTCTTTATGGTCAGCTTAAGTTTGGTACACTAGATTGTACAGTTCAT  
GAGGGACTCTGTAACATGTATAACATTGAGGCTTATCCAACAACAGTGGTATTCAACCAGTC  
CAACATTCATGAGTATGAAGGACATCACTCTGCTGAACAAATCTTGAGTTTCATAGAGGATC  
TTATGAATCCTTCAGTGGTCTCCCTTACACCCACCACCTTCAACGAACTAGTTACACAAAGA  
AAACACAACGAAGTCTGGATGGTTGATTTCTATTCTCCGTGGTGTATCCTTGCCAAGTCTT  
AATGCCAGAATGGAAAAGAATGGCCCGGACATTAAGTGGACTGATCAACGTGGGCAGTATAG  
ATTGCCAACAGTATCATTCTTTTTGTGCCAGGAAAACGTTCAAAGATACCCTGAGATAAGA  
TTTTTTCCCCCAAATCAAATAAAGCTTATCAGTATCACAGTTACAATGGTTGGAATAGGGA  
TGCTTATTCCCTGAGAATCTGGGGTCTAGGATTTTTACCTCAAGTATCCACAGATCTAACAC  
CTCAGACTTTTCAAGTAAAAAGTTCTACAAGGGAAAAATCATTGGGTGATTGATTTCTATGCT  
CCTTGGTGTGGACCTTGCCAGAATTTTGCTCCAGAATTTGAGCTCTTGGCTAGGATGATTAA  
AGGAAAAGTGAAAGCTGGAAAAGTAGACTGTCAGGCTTATGCTCAGACATGCCAGAAAGCTG  
GGATCAGGGCCTATCCAAGTGTAAAGTTTTATTTCTACGAAAGAGCAAAGAGAAATTTCAA  
GAAGAGCAGATAAATACCAGAGATGCAAAAGCAATCGCTGCCTTAATAAGTGAAAAATTGGA  
AACTCTCCGAAATCAAGGCAAGAGGAATAAGGATGAACTTTGAATAATGTTGAAGATGAAGAA  
AAAGTTTAAAAGAAATCTGACAGATGACATCAGAAGACACCTATTTAGAATGTTACATTTA  
TGATGGGAATGAATGAACATTATCTTAGACTTGCAAGTTGTACTGCCAGAATTATCTACAGCA  
CTGGTGTAAAAGAAGGGTCTGCAAACTTTTTCTGTAAAGGGCCGGTTTATAAATATTTTAGA  
CTTTGCAGGCTATAATATATGGTTCACACATGAGAACAAGAATAGAGTCATCATGTATTCTT  
TGTTATTTGCTTTTAAACAACCTTTAAAAAATATTTAAACGATTCTTAGCTCAGAGCCATACA  
AAAGTAGGCTGGATTGAGTCCATGGACCATAGATTGCTGTCCCCCTCGACGGACTTATAATG  
TTTCAGGTGGCTGGCTTGAACATGAGTCTGCTGTGCTATCTACATAAATGTCTAAGTTGTAT  
AAAGTCCACTTTCCCTTCACGTTTTTTGGCTGACCTGAAAAGAGGTAAGTTAGTTTTTGGTC  
ACTTGTTCTCCTAAAAATGCTATCCCTAACCATATATTTATATTTTCGTTTTTAAACACCCA  
TGATGTGGCACAGTAAACAAACCTGTTATGCTGTATTATTATGAGGAGATTCTTCATTGTT  
TTCTTTCTTCTCAAAGGTTGAAAAAATGCTTTTAATTTTTTACAGCCGAGAAACAGTGCAG

**FIGURE 189B**

CAGTATATGTGCACACAGTAAGTACACAAATTTGAGCAACAGTAAGTGCACAAATTCTGTAG  
TTTGCTGTATCATCCAGGAAAACCTGAGGGGAAAAAATTATAGCAATTAAGTGGGCATTGTA  
GAGTATCCTAAATATGTTATCAAGTATTTAGAGTTCTATATTTTAAAGATATATGTGTTTCAT  
GTATTTTCTGAAATTGCTTTCATAGAAATTTTCCCACTGATAGTTGATTTTGGAGGCATCTA  
ATATTTACATATTTGCCTTCTGAACCTTTGTTTTGACCTGTATCCTTTATTTACATTGGGTTT  
TTCTTTCATAGTTTTGGTTTTTCACTCCTGTCCAGTCTATTTATTATTCAAATAGGAAAAAT  
TACTTTACAGGTTGTTTTACTGTAGCTTATAATGATACTGTAGTTATTCCAGTTACTAGTTT  
ACTGTCAGAGGGCTGCCTTTTTTCAGATAAATATTGACATAATAACTGAAGTTATTTTTATAA  
GAAATCAAGTATATAAATCTAGGAAAGGGATCTTCTAGTTTCTGTGTTGTTTAGACTCAAA  
GAATCACAAATTTGTCAGTAACATGTAGTTGTTTAGTTATAATTCAGAGTGTACAGAATGGT  
AAAAATCCAATCAGTCAAAAGAGGTCAATGAATTAAAAGGCTTGCAACTTTTTTCAAAAAAA  
AAAAA



**FIGURE 190**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439  
<subunit 1 of 1, 747 aa, 1 stop  
<MW: 86127, pI: 7.46, NX(S/T): 2  
MGVWLNKDDYIRD LKRIILCFLIVYMAILVGT DQDFYSL LGVSKTASSREIRQA FKKLALKL  
HPDKNPNNPNAHGDF LKINRAYEVLKDEDLRKKYDKYGEK GLEDNQGGQYESWNYRYDFGI  
YDDDPEIITLERREFDA AVNSGELWFVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNC  
GDDRMLCRMKG VNSYP SLFTFRSGMAPVKYHGDRSKESLV SFAMQHVRSTVTELWTGNFVNS  
IQTAFAAGIGWLITFC SKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSAN  
TLEDRLAHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSNLYVFQP  
SLAVFKGQGTKEYEIH HGKKILYDILAFAKESVNSHVTT LGPQNFPANDKEPWLVDFFAPWC  
PPCRALLPELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSNIEYEGHHS  
AEQILEFIEDLMNPSVVSLTPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMART  
LTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLG  
FLPQVSTD LTPQTFSEKVLQGNHWVIDFYAPWCGPCQNFAP EFELLARMIKGKVKAGKVDC  
QAYAQTCQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKAI AALISEKLET LRNQGKRNKDEL

**Important features:**

Endoplasmic reticulum targeting sequence.

amino acids 744-747

Cytochrome c family heme-binding site signature.

amino acids 158-163

Nt-dnaJ domain signature.

amino acids 77-96

N-glycosylation site.

amino acids 484-487

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**FIGURE 191**

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAA  
GCCATGAACATCATCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGA  
GTCGTTGGTGAAGTTTTTCATTCCTCAGAGGAGAAAATCTGTGGCTGGGGAGATTGTTCTCA  
TTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC  
ATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAACTGCAGCTGAGTGCCGAAA  
ACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT  
CTCTAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA  
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA  
CATCCTAGGACATTTTTTGGATCACAAAAGCACTTCTTCCATCGATGATGGAGAGAAATCATG  
GCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGATTCCCTTACCTCATCCCATAT  
TGTTCCAGCAAATTTGCCGCTGTTGGCTTTCACAGAGGTCTGACATCAGAACTTCAGGCCTT  
GGGAAAAACTGGTATCAAAACCTCATGTCTCTGCCAGTTTTTGTGAATACTGGGTTCACCA  
AAAATCCAAGCACAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATA  
GATGGAATACTTACCAATAAGAAAATGATTTTTTGTTCATCGTATATCAATATCTTTCTGAG  
ACTACAGAAGTTTCTTCCTGAACGCGCCTCAGCGATTTTAAATCGTATGCAGAATATTCAAT  
TTGAAGCAGTGGTTGGCCACAAAATCAAAATGAAATGAATAAATAAGCTCCAGCCAGAGATG  
TATGCATGATAATGATATGAATAGTTTCGAATCAATGCTGCAAAGCTTTATTTACATTTTTT  
TCAGTCCTGATAATATTAAAAACATTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTA  
ATTACCTGTCTTCCTGTTTCTCAAGAATATTTACGTAGTTTTTTCATAGGTCTGTTTTTCCTT  
TCATGCCTCTTAAAAACTTCTGTGCTTACATAAACATACTTAAAAGGTTTTCTTTAAGATAT  
TTTATTTTTTCCATTTAAAGGTGGACAAAAGCTACCTCCCTAAAAGTAAATACAAAGAGAACT  
TATTTACACAGGGAAGGTTTAAGACTGTTCAAGTAGCATTCCAATCTGTAGCCATGCCACAG  
AATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT  
ATCTCAACCTGGACATATTTTAAGATTCAGCATTTGAAAGATTTCCCTAGCCTCTTCCTTTT  
TCATTAGCCCAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTAT  
AACTCTGAAGTCCACCAAAGTGGACCCTCTATATTTCCCTCCCTTTTTATAGTCTTATAAGA  
TACATTATGAAAGGTGACCGACTCTATTTTAAATCTCAGAATTTTAAGTTCTAGCCCCATGA  
TAACCTTTTTCTTTGTAATTTATGCTTTCATATATCCTTGGTCCCAGAGATGTTTAGACAAT  
TTTAGGCTCAAAAATTAAAGCTAACACAGGAAAAGGAACTGTACTGGCTATTACATAAGAAA  
CAATGGACCCAAGAGAAGAA

**FIGURE 192**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409  
<subunit 1 of 1, 300 aa, 1 stop  
<MW: 33655, pI: 9.31, NX(S/T): 1  
MNIILEILLLLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSI  
LVLWDINKRGVEETAAECRKLGVTAHAYVVDSCSNREEIYRSLNQVKKEVGDVTIVVNNAGTV  
YPADLLSTKDEEITKTFEVNILGHFWITKALLPSMMERNHGHIVTVASVCGHEGIPYLIPYC  
SSKFAAVGFHRGLTSELQALGKTGIKTSCLCPVFVNTGFTKNPSTRLWPVLETDEVVRSLID  
GILTNNKKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

Important features:

Signal peptide:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-33 and 58-61

Short-chain alcohol dehydrogenase family protein

amino acids 165-202, 37-49, 112-122 and 210-219

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**FIGURE 193**

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCACAGCAGG  
ATGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGCCAGCCCGCCCGGGGC  
AGGATGACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTCGGTGTTCATGATCCT  
GCTGATCATCGTGTACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGCACACGTCCTTCT  
CTAGGCCGCACACGGGGCCGCGCTGCCCACGCCCGGGCCGGACAGGGACAGGGAGCTCACG  
GCCGACTCCGATGTGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA  
CCTTCCCAGAAAGGAGACGGAGCAGCCGCCTGCGCCGGGGAGCATGGAGGAGAGCGTGAGAG  
GCTACGACTGGTCCCCGCGCGACGCCCGGCGCAGCCCAGACCAGGGCCGGCAGCAGGCGGAG  
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACTCCAGCCTGGCCTTCCCCACCAAGGAGCG  
CGCATTGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCGGCACGGGG  
CCATCTACTGCTACGTGCCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG  
AGCGGAAGCCTGCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCA  
CGTGCACAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCT  
CCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCCTCTTCGTGCGCGACCCC  
TTCGTGCGCCTGATCTCCGCCTTCCGCAGCAAGTTCGAGCTGGAGAACGAGGAGTTCTACCG  
CAAGTTCGCCGTGCCCATGCTGCGGCTGTACGCCAACACACCAGCCTGCCCGCCTCGGGCGC  
GCGAGGCCTTCCGCGCTGGCCTCAAGGTGTCCTTCGCCAACTTCATCCAGTACCTGCTGGAC  
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCA  
CCCGTGCCAGATCGACTACGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGC  
AGCTGCTGCAGCTACTCCAGGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGG  
ACCGCCAGCAGCTGGGAGGAGGACTGGTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT  
GTATAAACTCTACGAGGCCGACTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACCTCCTCC  
GAGACTGAAAGCTTTCGCGTTGCTTTTTCTCGCGTGCTGGAACCTGACGCACGCGCACTCC  
AGTTTTTTTATGACCTACGATTTTGCAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCC  
ATTGAGTACTGTATCGATATTGTTTTTTAAGATTAATATATTTTCAGGTATTTAATACGA

**FIGURE 194**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112

<subunit 1 of 1, 414 aa, 1 stop

<MW: 48414, pI: 9.54, NX(S/T): 4

MTKARLFRLWLVLGSMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRELT  
DSDVDEFLDKFELSAGVKQSDLPRKETEQPPAPGSMEESVRGYDWSPRDARRSPDQGRQQAER  
RSVLRGFCANSSLAFTKERAFFDDIPNSELHSLIVDDRHGAIYCYVPKVACTNWKRMIVLS  
GSLHHRGAPYRDPLRIPREHVHNASAHLTENKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPF  
VRLISAFRSKFELNEEFYRKFAVPMLRLYANHTSLPASAREAFRAGLKVSFANFIQYLLDP  
HTEKLAPFNEHWROVYRLCHPCQIDYDFVGKLETLDDEAAQLLQLLQVDRQLRFPPSYRNRT  
ASSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKPENLLRD

Important features:

Signal peptide:

amino acids 1-31

N-glycosylation sites.

amino acids 134-137, 209-212, 280-283 and 370-373

TNFR/NGFR family cysteine-rich region protein

amino acids 329-332

**FIGURE 195**

TCGGGCCAGAATTTCGGCACGAGGCGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA  
AAGAGGCCCAGAGTAGAGAGAGAGAGAGACCGACGTACACGGGATGGCTACGGGAACGCGCT  
ATGCCGGGAAGGTGGTGGTCGTGACCGGGGGCGGGCGCGGCATCGGAGCTGGGATCGTGCGC  
GCCTTCGTGAACAGCGGGGCCCCGAGTGGTTATCTGCGACAAGGATGAGTCTGGGGGCCGGGC  
CCTGGAGCAGGAGCTCCCTGGAGCTGTCTTTATCCTCTGTGATGTGACTCAGGAAGATGATG  
TGAAGACCCTGGTTTCTGAGACCATCCSCCGATTGCGCCGCTGGATTGTGTTGTCAACAAC  
GCTGGCCACCACCCACCCCCACAGAGGCCTGAGGAGACCTCTGCCCAGGGATTCCGCCAGCT  
GCTGGAGCTGAACCTACTGGGGACGTACACCTTGACCAAGCTCGCCCTCCCCTACCTGCGGA  
AGAGTCAAGGGAATGTCATCAACATCTCCAGCCTGGTGGGGGCAATCGGCCAGGCCCAGGCA  
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAGCTTTGGCCCTGGATGA  
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCCAGGAAACATCTGGACCCCGCTGTGGG  
AGGAGCTGGCAGCCTTAATGCCAGACCCTAGGGCCACAATCCGAGAGGGCATGCTGGCCCAG  
CCACTGGGCGCATGGGCCAGCCCGCTGAGGTGCGGGGCTGCGGCAGTGTTCTTGGCCTCCGA  
AGCCAACCTTCTGCACGGGCATTGAACTGCTCGTGACGGGGGGTGACAGAGCTGGGGTACGGGT  
GCAAGGCCAGTCGGAGCACCCCCGTGGACGCCCCCGATATCCCTTCCTGATTTCTCTCATTT  
CTACTTGGGGCCCCCTTCCTAGGACTCTCCACCCCCAACTCCAACCTGTATCAGATGCAGC  
CCCCAAGCCCTTAGACTCTAAGCCAGTTAGCAAGGTGCCGGGTACCCTGCAGGTTCCCAT  
AAAAACGATTTGCAGCC

**FIGURE 196**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045

<subunit 1 of 1, 270 aa, 1 stop

<MW: 28317, pI: 6.00, NX(S/T): 1

MATGTRYAGKVVVVTGGGRGIGAGIVRAFNNSGARVVICDKDESGGRALEQELPGAVFILCD  
VTQEDDVKTLVSETIRRFGRLCDVNNAGHHPPQRPETSAQGFRQLLELNLLGTYTLTKL  
ALPYLRKSQGNVINISSLVGAIGQAQAVPYVATKGAVTAMTKALALDESPYGVRVNCISPGN  
IWTPLWEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAAVFLASEANFCTGIELLVTTGG  
AELGYGCKASRSTPVDAPDIPS

Important features:

N-glycosylation site.

amino acids 138-141

Short-chain alcohol dehydrogenase family protein

amino acids 10-22, 81-91, 134-171 and 176-185

**FIGURE 197**

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGGA CTGGCCTCACAACCTG  
CTGTTTCTTCTTACCATTTCATCTTCCTGGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAA  
GAGGAAGGGGCAAGGGCGGCCTGGGCCCCCTGGCCCCCTGGCCCTCACCAGGTGCCACTGGACC  
TGGTGTCACGGATGAAACCGTATGCCCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATG  
GTGGCCCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGTCAACTTGCAGCT  
GTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCCAGCC  
GTATCCCCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGTGAACCCCTTCACC  
ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTCAGCCAGGTTCCTGTGCGCCGCCG  
CCTCTGCCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCG  
CTGTGGGCTGCACCTGCATCTTCTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCCGAGA  
CCATCCTCCTTGCACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAA  
GCAAG



**FIGURE 198**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59294

<subunit 1 of 1, 180 aa, 1 stop

<MW: 20437, pI: 9.58, NX(S/T): 1

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKQGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEY  
ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPRIIPVDLPEARCLCL  
GCVNPFTMQEDRSMVSVPVFSQVPVRRRLCPPPPRTGPCRQRAVMETIAVGCTCIF

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 75-78

Homologous region to IL-17

amino acids 96-180.

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**FIGURE 199**

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCCTTGAAAAACCCGGCGGG  
CGAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCACACTCCCCGCCGAGAAGCCTCGCTCG  
GCGCCCAACATGGCGGGTGGGCGCTGCGGCCCCGAGCTAACGGCGCTCCTGGCCGCCTGGAT  
CGCGGCTGTGGCGGCGACGGCAGGCCCCGAGGAGGCCGCGCTGCCGCCGAGCAGAGCCGGG  
TCCAGCCCATGACCGCCTCCAACCTGGACGCTGGTGATGGAGGGCGAGTGATGCTGAAATTT  
TACGCCCCATGGTGTCATCCTGCCAGCAGACTGATTCAGAATGGGAGGCTTTTGCAAAGAA  
TGGTGAAATACTTCAGATCAGTGTTGGGAAGGTAGATGTCATTCAAGAACCAGGTTTGAGTG  
GCCGCTTCTTTGTCACTACTCTCCAGCATTTTTTTCATGCAAAGGATGGGATATTCCGCCGT  
TATCGTGGCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATC  
AGTCGAGCCTCTGACTGGCTGGAAATCCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTC  
TTTTTAGCATCTCTGGCAAGATATGGCATCTTCACAACTATTTACAGTGACTCTTGGAATT  
CCTGCTTGGTGTTCTTATGTGTTTTTCGTATAGCCACCTTGGTTTTTGGCCTTTTTATGGG  
TCTGGTCTTGGTGGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGC  
GTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAG  
GAGGAAAAAGATGATTCAAATGAAGAAGAAACAAAGACAGCCTTGTAGATGATGAAGAAGA  
GAAAGAAGATCTTGGCGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACCTTGGCTG  
CTGGTGTGGATGAGGAGAGAAGTGAGGCCAATGATCAGGGGCCCCCAGGAGAGGACGGTGTG  
ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCCTGCCAGC  
TGACACAGAGGTGGTGGAAGACTCCTTGAGGCAGCGTAAAAGTCAGCATGCTGACAAGGGAC  
TGTAGATTTAATGATGCGTTTTCAAGAATACACACCAAAACAATATGTCAGCTTCCCTTTGG  
CCTGCAGTTTGTACCAAATCCTTAATTTTTTCCTGAATGAGCAAGCTTCTCTTAAAGATGCT  
CTCTAGTCATTTGGTCTCATGGCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGT  
GACAATCAGGATATAGAAAAACAAACGTAGTGTTGGGATCTGTTTGGAGACTGGGATGGGAA  
CAAGTTCATTTACTTAGGGGTCAGAGAGTCTCGACCAGAGGAGGCCATTCCCAGTCCTAATC  
AGCACCTTCCAGAGACAAGGCTGCAGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTTGGCT  
CCTGAGCATCCCCAAAGTGTAACGTAGAAGCCTTGATCCTTTTCTTGTGTAAAGTATTTAT  
TTTTGTCAAATTGCAGGAAACATCAGGCACCACAGTGCATGAAAAATCTTTACAGCTAGAA  
ATTGAAAGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCCAGCCCTCTGAATCTCCTG  
TGCTATGTTTTATTTCTTACCTTTAATTTTTCCAGCATTTCCACCATGGGCATTCAGGCTCT  
CCACACTCTTCACTATTATCTCTTGGTCAGAGGACTCCAATAACAGCCAGGTTTACATGAAC  
TGTGTTTGTTCATTCTGACCTAAGGGGTTTAGATAATCAGTAACCATAACCCCTGAAGCTGT  
GACTGCCAAACATCTCAAATGAAATGTTGTGGCCATCAGAGACTCAAAGGAAGTAAGGATT  
TTACAAGACAGATTAAAAAAAATTGTTTTGTCCAAAATATAGTTGTTGTTGATTTTTTTTT  
AAGTTTTCTAAGCAATATTTTTCAAGCCAGAAGTCTCTAAGTCTTGCCAGTACAAGGTAGT  
CTTGTGAAGAAAAGTTGAATACTGTTTTGTTTTTCATCTCAAGGGGTTCCCTGGGTCTTGAAC  
TACTTTAATAATAACTAAAAAACCACTTCTGATTTTCTTCAGTGATGTGCTTTTGGTGAAA  
GAATTAATGAACCTCAGTACCTGAAAGTGAAAGATTTGATTTTGTTCATCTTCTGTAAATC  
TTCCAAAGAATTATATCTTTGTAAATCTCTCAATACTCAATCTACTGTAAGTACCCAGGGAG  
GCTAATTTCTTT

**FIGURE 200**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56433  
<subunit 1 of 1, 349 aa, 1 stop  
<MW: 38952, pI: 4.34, NX(S/T): 1  
MAGGRCGPQLTALLAAWIAAVAATAGPEEAALPPEQSRVQPMTASNWTLVMEGEWMLKFYAP  
WCPSCQQT DSEWEAFAKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGI FRRYRG  
PGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAW  
CSYVFFVIATLVFGLFMGLVLVVISSECFYVPLPRHLSEERSEQNRRSEEAHRAEQLQDAEEEEK  
DDSNEEENKDSLVDDEEEKEDLGDEDEAEDEEEEDNLAAGVDEERSEANDQGPPGEDGV TRE  
EVEPEEAEEGISEQPCPADTEVVEDSLRQRKSQHADKGL

**Important features:****Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 191-211

**N-glycosylation site.**

amino acids 46-49

**Thioredoxin family proteins. (homologous region to disulfide isomerase)**

amino acids 56-72

**Flavodoxin proteins**

amino acids 173-187

**FIGURE 201**

ATCTGGTTGAACTACTTAAGCTTAATTTGTTAAACTCCGGTAAGTACCTAGCCACATGATT  
TGAATCAGAGATTCTCTTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAAGAGCTCC  
CAAATGCTATATCTATTTCAGGGGCTCTCAAGAACAATGGAATATCATCCTGATTTAGAAAAT  
TTGGATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAATACCAGGATAGCTGT  
TGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTCATTGCTGTAATTTTGG  
GAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCCTGGGTACCATGGGGGTTCTTTCC  
AGCCCTTGTCTCTTAATTGGATTATATATGAGAAGAGCTGTTATCTATTTCAGCATGTCACT  
AAATTCCTGGGATGGAAGTAAAAGACAATGCTGGCAACTGGGCTCTAATCTCCTAAAGATAG  
ACAGCTCAAATGAATTGGGATTTATAGTAAAACAAGTGTCTTCCCAACCTGATAATTCATTT  
TGGATAGGCCTTTCTCGGCCCCAGACTGAGGTACCATGGCTCTGGGAGGATGGATCAACATT  
CTCTTCTAACTTATTTTCAGATCAGAACCACAGCTACCCAAGAAAACCCATCTCCAAATTGTG  
TATGGATTACAGTGTGAGTCATTTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGT  
GAGAAGAAGTTTTCAATGTAAGAGGAAGGGTGGAGAAGGAGAGAGAAATATGTGAGGTAGTA  
AGGAGGACAGAAAACAGAACAGAAAAGAGTAACAGCTGAGGTCAAGATAAATGCAGAAAATG  
TTTAGAGAGCTTGGCCAACCTGTAATCTTAACCAAGAAATTGAAGGGAGAGGCTGTGATTTCT  
GTATTTGTGACCTACAGGTAGGCTAGTATTATTTTTCTAGTTAGTAGATCCCTAGACATGG  
AATCAGGGCAGCCAAGCTTGAGTTTTTATTTTTTATTTATTTTATTTTGTAGATAGGGTCT  
CACTTTGTTACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGCTATCTCTCGC  
CTCAGCCCCCTCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTTGGTG  
TTTTTTGTAGAGACTGGGTTTTGCCATGTTGACCAAGCTGGTCTCTAACTCCTGGGCTTAAG  
TGATCTGCCCCGCTTGGCCTCCCAAGTGCTGGGATTACAGATGTGAGCCACCACACCTGGC  
CCCAAGCTTGAATTTTCTATTCTGCCATTGACTTGGCATTACCTTGGGTAAGCCATAAGCGA  
ATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGCACGGT  
GTGTTGCCACGATTTGACCCTCAACTTCTAGCAGTATATCAGTTATGAACTGAGGGTGAAAT  
ATATTTCTGAATAGCTAAATGAAGAAATGGGAAAAAATCTTCACCACAGTCAGAGCAATTTT  
ATTATTTTCATCAGTATGATCATAATTATGATTATCATCTTAGTAAAAAGCAGGAACTCCTA  
CTTTTTCTTTATCAATTAAATAGCTCAGAGAGTACATCTGCCATATCTCTAATAGAATCTTT  
TTTTTTTTTTTTTTTTTTTTTGTAGACAGAGTTTCGCTCTTGTGCCCAGGCTGGAGTGAACGG  
CACGATCTCGGCTCACCGCAACCTCCGCCCCCTGGGTTCAAGCAATTCTCCTGCCTCAGCCT  
CCCAAGTAGCTGGGATTACAGTCAGGCACCACCACACCCGGCTAATTTTGTATTTTTTTAGT  
AGAGACAGGGTTTCTCCATGTGCGTCAAGGTAGTCCCGAACTCCTGACCTCAAGTGATCTGC  
CTGCCTCGGCCTCCCAAGTGCTGGGATTACAGGCGTGAGCCACTGCACCCAGCCTAGAATCT  
TGTATAATATGTAATTGTAGGGAACTGCTCTCATAGGAAAGTTTTCTGCTTTTTTAAATACA  
AAAAATACATAAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACCTCATTGGA  
ACAAGTATTAACATTTTGAATATGTTTTATTAGTTTTGTGATGTACTGTTTTACAATTTTT  
ACCATTTTTTTTCAGTAATTACTGTAAAATGGTATTATTGGAATGAACTATATTTCTCATG  
TGCTGATTTGTCTTATTTTTTTTCTACTTTCCCACTGGTGCTATTTTTATTTCCAATGGATA  
TTTCTGTATTACTAGGGAGGCATTTACAGTCCTCTAATGTTGATTAAATATGTGAAAAGAAAT  
TGTACCAATTTTACTAAATTATGCAGTTTAAATGGATGATTTTATGTTATGTGGATTTTCAT  
TTCAATAAAAAAAACTCTTATCAAAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTT

**FIGURE 202**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912

<subunit 1 of 1, 201 aa, 1 stop

<MW: 22563, pI: 4.87, NX(S/T): 1

MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGSAAASPPWRLIAVILGILCLVILVIAV  
VLGTMGVLSSPCPPNWIIYEKSCYLFSMSLNSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQ  
VSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL  
CSVPSYSICEKKFSM

**Important features:**

Type II transmembrane domain:

amino acids 45-65

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 197-200

N-myristoylation sites.

amino acids 35-40 and 151-156

Homologous region to LDL receptor

amino acids 34-67 and 70-200.

GGAAGGGGAGGAGCAGGCCACACAGGCACAGGCCGGTGAGGGACCTGCCCAGACCTGGAGGG  
TCTCGCTCTGTACACAGGCTGGAGTGCAGTGGTGTGATCTTGGCTCATCGTAACCTCCACC  
TCCCGGGTTCAAGTGATTCTCATGCCTCAGCCTCCCGAGTAGCTEGGATTACAGGTGGTGAC  
TTCCAAGAGTGACTCCGTCGGAGGAAAATGACTCCCCAGTCGCTGCTGCAGACGACACTGTT  
CCTGCTGAGTCTGCTCTTCCCTGGTCCAAGGTGCCACCGGCAGGGGCCACAGGGAAGACTTTC  
GCTTCTGCAGCCAGCGGAACCAGACACACAGGAGCAGCCTCCACTACAAACCCACACCAGAC  
CTGCGCATCTCCATCGAGAACTCCGAAGAGGGCCCTCACAGTCCATGCCCTTTCCCTGCAGC  
CCACCCTGCTTCCCGATCCTTCCCTGACCCCAAGGGCCCTCTACCACTTCTGCCTCTACTGGA  
ACCGACATGCTGGGAGATTACATCTTCTCTATGGCAAGCGTGACTTCTTGCTGAGTGACAAA  
GCCTCTAGCCTCCTCTGCTTCCAGCACCAGGAGGAGAGCCTGGCTCAGGGCCCCCGCTGTT  
AGCCACTTCTGTACCTCCTGGTGGAGCCCTCAGAACATCAGCCTGCCCAGTGCCGCCAGCT  
TCACCTTCTCCTTCCACAGTCCTCCCCACACGGCCGCTCACAATGCCTCGGTGGACATGTGC  
GAGCTCAAAAGGGACCTCCAGCTGCTCAGCCAGTTCTGAAGCATCCCCAGAAGGCCTCAAG  
GAGGCCCTCGGCTGCCCCCGCCAGCCAGCAGTTGCAGAGCCTGGAGTCGAAACTGACCTCTG  
TGAGATTATGAGGGGACATGGTGTCTTCGAGGAGGACCGGATCAACGCCACGGTGTGGAAG  
CTCCAGCCACAGCCGGCCTCCAGGACCTGCACATCCACTCCCGGCAGGAGGAGGAGCAGAG  
CGAGATCATGGAGTACTCGGTGCTGCTGCCTCGAACACTCTTCCAGAGGACGAAAGGCCGGA  
GCGGGGAGGCTGAGAAGAGACTCCTCCTGGTGGACTTCAGCAGCCAAGCCCTGTTCCAGGAC  
AAGAATTCCAGCCAAGTCCTGGGTGAGAAGGTCTTGGGGATTGTGGTACAGAACACCAAAGT  
AGCCAACCTCACGGAGCCCGTGGTGTCTACTTTCCAGCACCAGCTACAGCCGAAGAATGTGA  
CTCTGCAATGTGTGTTCTGGGTGAAGACCCACATTGAGCAGCCCGGGGCATTGGAGCAGT  
GCTGGGTGTGAGACCGTCAGGAGAGAAACCCAAACATCCTGCTTCTGCAACCACTTGACCTA  
CTTTGCAGTGCTGATGGTCTCCTCGGTGGAGGTGGACGCCGTGCACAAGCACTACCTGAGCC  
TCCTCTCCTACGTGGGCTGTGTCTCTGCCCTGGCCTGCCTTGTACCACTTGCCGCCTAC  
CTCTGCTCCAGGGTGCCCTGCCGTGCAGGAGGAAACCTCGGGACTACACCATCAAGGTGCA  
CATGAACCTGCTGCTGGCCGTCTTCTGCTGGACACGAGCTTCCTGCTCAGCGAGCCGGTGG  
CCCTGACAGGCTCTGAGGCTGGCTGCCGAGCCAGTGCCATCTTCTGCACTTCTCCCTGCTC  
ACCTGCCTTTCTGATGGGCTCGAGGGGTACAACCTCTACCGACTCGTGGTGGAGGTCTT  
TGGCACCTATGTCCCTGGCTACCTACTCAAGCTGAGCGCCATGGGCTGGGGCTTCCCCATCT  
TTCTGGTGACGCTGGTGGCCCTGGTGGATGTGGACAACCTATGGCCCCATCATCTTGGCTGTG  
CATAGGACTCCAGAGGGCGTCATCTACCTTCCATGTGCTGGATCCGGGACTCCCTGGTCAG  
CTACATCACCAACCTGGGCTCTTCAGCCTGGTGTCTTCTGTTCAACATGGCCATGCTAGCCA  
CCATGGTGGTGCAGATCCTGCGGCTGCGCCCCCACACCCAAAAGTGGTCACATGTGCTGACA  
CTGCTGGGCTCAGCCTGGTCTTGGCCTGCCCTGGGCTTGATCTTCTTCTCCTTTGCTTC  
TGGCACCTTCCAGCTTGTGCTCCTCTACCTTTTCAGCATCATCACCTCCTTCCAAGGCTTCC  
TCATCTTCATCTGGTACTGGTCCATGCGGCTGCAGGCCCGGGGTGGCCCTCCCCCTCTGAAG  
AGCAACTCAGACAGCGCCAGGCTCCCCATCAGCTCGGGCAGCACCTCGTCCAGCCGCATCTA  
GGCCTCCAGCCCACCTGCCCATGTGATGAAGCAGAGATGCGGCCTCGTCGCACACTGCCTGT  
GGCCCCCGAGCCAGGCCAGCCCCAGGCCAGTCAGCCGCAGACTTTGGAAAGCCCAACGACC  
ATGGAGAGATGGGCCGTTGCCATGGTGGACGGACTCCCGGGCTGGGCTTTTGAATTGGCCTT  
GGGGACTACTCGGCTCTCACTCAGCTCCACGGGACTCAGAAGTGCGCCGCCATGCTGCCTA  
GGGTACTGTCCCCACATCTGTCCCAACCCAGCTGGAGGCCTGGTCTCTCCTTACAACCCCTG  
GGCCCAGCCCTCATTGCTGGGGGCCAGGCCTTGGATCTTGAGGGTCTGGCACATCCTTAATC  
CTGTGCCCTGCCTGGGACAGAAATGTGGCTCCAGTTGCTCTGTCTCTCGTGGTCAACCCTGA  
GGGCACTCTGCATCCTCTGTCAATTTTAACCTCAGGTGGCACCCAGGGCGAATGGGGCCCAGG  
GCAGACCTTCAGGGCCAGAGCCCTGGCGGAGGAGAGGCCCTTTGCCAGGAGCACAGCAGCAG  
CTCGCCTACCTCTGAGCCCAGGCCCCCTCCCTCCCTCAGCCCCCAGTCCTCCCTCCATCTT  
CCCTGGGGTTCTCCTCCTCTCCAGGGCCTCCTTGCTCCTTCGTTACAGCTGGGGGTCCCC  
GATTCCAATGCTGTTTTTTGGGGAGTGGTTTTCCAGGAGCTGCCTGGTGTCTGCTGTAAATGT  
TTGTCTACTGCACAAGCCTCGGCCTGCCCTGAGCCAGGCTCGGTACCGATGCGTGGGCTGG  
GCTAGGTCCCTCTGTCCATCTGGGCCTTTGTATGAGCTGCATTGCCCTTGCTCACCTGACC  
AAGCACACGCCTCAGAGGGGCCCTCAGCCTCTCTGAAGCCCTCTTGTGGCAAGAACTGTGG  
ACCATGCCAGTCCCGTCTGGTTTTCCATCCCACCACTCCAAGGACTGAGACTGACCTCCTCTG  
GTGACACTGGCCTAGAGCCTGACACTCTCCTAAGAGGTTCTCTCCAAGCCCCCAAATAGCTC



**FIGURE 203B**

CAGGCGCCCTCGGCCGCCCATCATGGTTAATTCTGTCCAACAAACACACACGGGGTAGATTGC  
TGGCCTGTTGTAGGTGGTAGGGACACAGATGACCGACCTGGTCACTCCTCCTGCCAACATTC  
AGTCTGGTATGTGAGGCGTGCGTGAAGCAAGAACTCCTGGAGCTACAGGGACAGGGAGCCAT  
CATTCCTGCCTGGGAATCCTGGAAGACTTCCTGCAGGAGTCAGCGTTCAATCTTGACCTTGA  
AGATGGGAAGGATGTTCTTTTACGTACCAATTCTTTTGTCTTTTGATATTAAAAAGAAGTA  
CATGTTCAATTGTAGAGAATTTGGAACTGTAGAAGAGAATCAAGAAGAAAAATAAAAAATCAG  
CTGTTGTAATCGCCTAGCAA  
AA



**FIGURE 204**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921  
<subunit 1 of 1, 693 aa, 1 stop  
<MW: 77738, pI: 8.87, NX(S/T): 7  
MTPQSLLQTTFLLSLLFLVQGAHGRGHREDFRFCSQRNQTHRSSLHYKPTPDLRISIENSE  
EALTVHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLLSDKASSLLCFQH  
QEESLAQGPPLLATSVTSWWSPQNISLPSAASFTFSFHSPHTAAHNASVDMCELKRDLQLL  
SQFLKHPQKASRRPSAAPASQQLOSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQD  
LHIHSRQEEEQSEIMEYSVLLPRTLFTQRTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGE  
KVLGIVVQNTKVANLTEPVVLTFOHQLOPKNVTLCVFWVEDPTLSSPGHWSSAGCETVRRE  
TQTSCFCNHLTYFAVLMVSSVEVDAVHKHYLSLLSYVGCVVSALACLVTIAAYLCSRVPPLPC  
RRKPRDYTIKVHMNLLLAVFLLDTSFLLSEPVALTGSEAGCRASAIFLHFSLLTCLSWMGLE  
GYNLYRLVVEVFGTYVPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPIILAVHRTPEGVIY  
PSMCWIRDSLVSYITNLGLFSLVLEFNMAMLATMVVQILRLRPHTQKWSHVLTLGLSLVLG  
LPWALIFFSFASGTFQLVVLYLFSIITSFQGFLIFIWYWSMRLQARGGPSPLKSNSDSARLP  
ISSGSTSSSRI

**Important features:****Signal peptide:**

amino acids 1-25

**Putative transmembrane domains:**amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590  
and 634-657**Microbodies C-terminal targeting signal.**

amino acids 691-693

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 198-201 and 370-373

**N-glycosylation sites.**amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327  
and 341-344**G-protein coupled receptors family 2 proteins**

amino acids 475-504

211/237

**FIGURE 205**

TGCCTGGCCTGCCTTGTCAACAATGCCGCTTACTCTGCTTCCAGGTGCCCCTGCCTTGCAGA  
GGAAANCNTCGGGACTACACCNTCAAGTGCACATGAACCTGCTGCTGGCCGTCTTCCTGCTG  
GACACGAGCTTCCTGCTCAGCGNAGCCGGTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA  
GCCAGTGCCATCTTCCTGCACTTCTCCTGCTCACCTGCCTTTCCTGGATGGGCCTCGAGGGG  
TACAACCTCTACCGACTCGTGGTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAA  
GCTGAGCGCCATGGGCTGGGGCTTCCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATG  
TGGACAACCTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCCT  
TCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACCAACCTGGGCCTCTTCAGCCT  
GGTGTTCCTGTTCAACATGG

**FIGURE 206**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTCAGGTCCA  
GGTTTTGCTTTGATCCTTTTCAAAAACCTGGAGACACAGAAGAGGGCTCTAGGAAAAAGTTTT  
GGATGGGATTATGTGGAACTACCTGCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCC  
ACCCAGTGCAGCCTTCCCCTGGCGGTGGTGAAAGAGACTCGGGAGTCGCTGCTTCCAAAGT  
GCCCCCGGTGAGTGAGCTCTCACCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGCT  
GACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTAAAT  
TCCAGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTATT  
ACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAAGAAATAC  
GGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACCTACGTTTGATG  
AAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTTGTAGAAGTTGAG  
GAACCCAGTGATGGAACCTATATTAGGGCGCTGGTGTGGTTCTGGTACTGTACCAGGAAAACA  
GATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCCTTCTGAAC  
CAGGGTTCTGCATCCACTACAACATTGTCTATGCCACAATTCACAGAAGCTGTGAGTCCTTCA  
GTGCTACCCCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGTAC  
CTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGATGGCAGTTGGACTTAGAAGATCTAT  
ATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTTTTTTGGGAAGAAAATCCAGAGTGGTG  
GATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGT  
GTCCATAAGGGAAGAATAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTA  
AACGCTGTGGTGGGAACTGTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCA  
AGCAAAGTTACTAAAAAATACCACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTCAGGGG  
ATTGCACAAATCACTCACCGACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCA  
GAGGGAGCACAGGAGGATAGCCGCATCACACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGC  
AGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTT  
CAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATT  
AGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATC  
GTGGAAAGAAAATTAATGTTGTATTAAATAGATCACAGCTAGTTTCAGAGTTACCATGTA  
CGTATTCCACTAGCTGGGTTCTGTATTTTCAGTTCTTTTCGATACGGCTTAGGGTAATGTCAGT  
ACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACCTCTAAAGCTCC  
ATGTCCTGGGCCTAAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTGCTCATATTCAC  
ATATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTTTAAAAGGAACCTATGTTGCT  
ATGAATTAACTTGTGTCTATGCTGATAGGACAGACTGGATTTTTTCATATTTCTTATTAAAT  
TTCTGCCATTTAGAAGAAGAGAATACTACATTCATGGTTTGGGAAGAGATAAACCTGAAAAGAAG  
AGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTAT  
ATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTAAATATATCTATTTTAC  
CAAAGGTATTTAATATTCTTTTTTTATGACAACTTAGATCAACTATTTTGTAGCTTGGTAAATT  
TTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGAC  
AAAAATACATGTATTTCACTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAA  
CTGAATTGGAATAGAATTGGTAAGTTGCAAAGACTTTTGGAAAATAATTAAATTATCATATC  
TTCCATTCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGAAAGTAGACATTCAGATCC  
AGCCATTACTAACCTATTCTTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACATAAAGC  
ACCTTGAAAAAGACTTGGCAGCTTCTGATAAAGCGTGCTGTGCTGTGCAGTAGGAACACAT  
CCTATTTATTGTGATGTTGTGGTTTTATTATCTTAAACTCTGTTCCATACACTTGTATAAAT  
ACATGGATATTTTTATGTACAGAAGTATGTCTCTTAACCAGTTCAGTTATTGTACTCTGGCA  
ATTTAAAAGAAAATCAGTAAAATATTTTGCTTGTAATGCTTAATATNGTGCCTAGGTTAT  
GTGGTGACTATTTGAATCAAAAATGTATTGAATCATCAATAAAAGAATGTGGCTATTTTG  
GGAGAAAATTAATAAAAAAAAAAAAAAAAAAAGGTTTAGGGATAACAGGGTAATGCGGCC

**FIGURE 207**

MSLFGLLLLT SALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPR  
FPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDG TILGRWC  
GSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLL  
NNAITAFSTLEDLIRYLEPERWQOLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL L TEEVRLY  
SCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVP SKVTKKYHEVLQ  
LRPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG

**FIGURE 208**

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACCAGACCTCTACATT  
CCATTTTGGAGAAGACTAAAAATGGTGTTTCCAATGTGGACACTGAAGAGACAAATTCTTA  
TCCTTTTAAACATAATCCTAATTTCCAAACTCCTTGGGGCTAGATGGTTTCTTAAACTCTG  
CCCTGTGATGTCACTCTGGATGTTCCAAAGAACCATGTGATCGTGGACTGCACAGACAAGCA  
TTTGACAGAAATTCTTGGAGGTATTCCCACGAACACCACGAACCTCACCTCACCATTAAACC  
ACATACCAGACATCTCCCCAGCGTCCTTTCACAGACTGGACCATCTGGTAGAGATCGATTTC  
AGATGCAACTGTGTACCTATTCCACTGGGGTCAAAAAACAACATGTGCATCAAGAGGCTGCA  
GATTAAACCCAGAAGCTTTAGTGGACTCACTTATTTAAATCCCTTTACCTGGATGGAAACC  
AGCTACTAGAGATACCGCAGGGCCTCCCGCCTAGCTTACAGCTTCTCAGCCTTGAGGCCAAC  
AACATCTTTTCCATCAGAAAAGAGAATCTAACAGAACTGGCCAACATAGAAATACTCTACCT  
GGGCCAAACTGTTATTATCGAAATCCTTGTTATGTTTCATATTCAATAGAGAAAGATGCCT  
TCCTAAACTTGACAAAGTTAAAGTGCTCTCCCTGAAAGATAACAATGTCACAGCCGTCCCT  
ACTGTTTTGCCATCTACTTTAACAGAACTATATCTCTACAACAACATGATTGCAAAAATCCA  
AGAAGATGATTTTAAATAACCTCAACCAATTACAAATTCTTGACCTAAGTGGAAATTGCCCTC  
GTTGTTATAATGCCCCATTTCCCTTGTCGCGCGTGTAATAAATAATTCTCCCTACAGATCCCT  
GTAAATGCTTTTGATGCGCTGACAGAATTAAAGTTTTACGTCTACACAGTAACTCTCTTCA  
GCATGTGCCCCCAAGATGGTTTAAAGAACATCAACAAACTCCAGGAACCTGGATCTGTCCCAA  
ACTTCTTGGCCAAAGAAATTGGGGATGCTAAATTTCTGCATTTTCTCCCCAGCCTCATCCAA  
TTGGATCTGTCTTTCAATTTTGAACCTCAGGTCTATCGTGCATCTATGAATCTATCACAAGC  
ATTTTCTTCACTGAAAAGCCTGAAAATTCTGCGGATCAGAGGATATGTCTTTAAAGAGTTGA  
AAAGCTTTAACCTCTCGCCATTACATAATCTTCAAAATCTTGAAGTTCTTGATCTTGGCACT  
AACTTTATAAAAATTGCTAACCTCAGCATGTTTAAACAATTTAAAAGACTGAAAGTCATAGA  
TCTTTCAGTGAATAAAATATCACCTTCAGGAGATTCAAGTGAAGTTGGCTTCTGCTCAAATG  
CCAGAACTTCTGTAGAAAGTTATGAACCCAGGTCTTGGACAATTACATTATTTAGATAT  
GATAAGTATGCAAGGAGTTGCAGATTCAAAAACAAAGAGGCTTCTTTCATGTCTGTTAATGA  
AAGCTGCTACAAGTATGGGCAGACCTTGGATCTAAGTAAAAATAGTATATTTTTTGTCAAGT  
CCTCTGATTTTTCAGCATCTTTCTTTCTTCAAATGCCTGAATCTGTCAGGAAATCTCATTAGC  
CAAACCTCTTAATGGCAGTGAATTTCAACCTTTAGCAGAGCTGAGATATTTGGACTTCTCCAA  
CAACCGGCTTGATTTACTCCATTCAACAGCATTGTAAGAGCTTCACAAACTGGAAGTTCTGG  
ATATAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTACTCATATGCTAAACTTTACC  
AAGAACCTAAAGGTTCTGCAGAACTGATGATGAACGACAATGACATCTCTTCCCTCCACCAG  
CAGGACCATGGAGAGTGAGTCTCTTAGAACTCTGGAATTCAGAGGAAATCACTTAGATGTTT  
TATGGAGAGAAGGTGATAACAGATACTTACAATTATTCAAGAATCTGCTAAAATTAGAGGAA  
TTAGACATCTCTAAAAATTCCTAAGTTTCTTGCCCTTCTGGAGTTTTTGTGATGGTATGCCTCC  
AAATCTAAAGAATCTCTCTTTGGCCAAAAATGGGCTCAAATCTTTCAGTTGGAAGAACTCC  
AGTGTCTAAAGAACCTGGAACTTTGGACCTCAGCCACAACCAACTGACCACTGTCCCTGAG  
AGATTATCCAACCTGTTCCAGAAGCCTCAAGAATCTGATTCTTAAGAATAATCAAATCAGGAG  
TCTGACGAAGTATTTTCTACAAGATGCCTTCCAGTTGCGATATCTGGATCTCAGCTCAAATA  
AAATCCAGATGATCCAAAAGACCAGCTTCCCAGAAAATGTCCTCAACAATCTGAAGATGTTG  
CTTTTGCATCATAATCGGTTTCTGTGCACCTGTGATGCTGTGTGGTTTGTCTGGTGGGTAA  
CCATACGGAGGTGACTATTCTTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGAGCAC  
ACAAGGGCCAAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTG  
ATTCTGTTCTCACTTTCCATATCTGTATCTCTCTTTCTCATGGTGTGATGACAGCAAGTCA  
CCTCTATTTCTGGGATGTGTGGTATATTTACCATTTCTGTAAGGCCAAGATAAAGGGGTATC  
AGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTTATTGTGTATGACACTAAAGACCCA  
GCTGTGACCGAGTGGGTTTTGGCTGAGCTGGTGGCCAACTGGAAGACCCAAGAGAGAAACA  
TTTTAATTTATGTCTCGAGGAAAGGGACTGGTTACCAGGGCAGCCAGTTCTGGAAAACCTTT  
CCCAGAGCATAACAGCTTAGCAAAAAGACAGTGTGTTGTGATGACAGACAAGTATGCAAAGACT  
GAAAATTTTAAAGATAGCATTCTTACTTGTCCCATCAGAGGCTCATGGATGAAAAAGTTGATGT  
GATTATCTTGATATTTCTTGAGAAGCCCTTTCAGAAGTCCAAGTTCCTCCAGCTCCGGAAAA  
GGCTCTGTGGGAGTTCTGTCTTGAGTGGCCAAACAAACCCGCAAGCTCACCCATACTTCTGG  
CAGTGTCTAAAGAACGCCCTGGCCACAGACAATCATGTGGCCTATAGTCAGGTGTTCAAGGA  
AACGGTCTAGCCCTTCTTTGCAAAACACAACCTGCCTAGTTTACCAAGGAGAGGCCTGGC



**FIGURE 209**

MVFPMWTLKRQILILFNIILISKLLGARWFPKTLPCDVTLDVDPKNHVIVDCTDKHLTEIPGG  
IPTNTTNLTLTINHIPDISPASFHRLDHLVEIDFRNCNCVPIPLGSKNNMCIKRLQIKPRSFS  
GLTYLKSLYLDGNQLLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLGQNCYR  
NPCYVSYSEKDAFLNLTKLKVLSLKDNNVTAVPTVLPSTLTELYLYNNMIAKIQEDDFNNL  
NQLQILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPPRWF  
KNINKLQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSLKSL  
KILRIRGYVFKELKSFNLSPLHNLQNLVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKIS  
PSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGO  
TLDLSKNSIFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNRLDLLH  
STAFEELHKLEVLDISSNSHYFQSEGITHMLNFTKNLKVLOKLMMNDNDISSSTSRTMESES  
LRTLEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNLSLSFLPSGVFDGMPPNLKNLSL  
AKNGLKFSWKKLQCLKNLETLDLSHNQLTTVPERLSNCSRSLSKNLILKNNQIRSLTKYFLQ  
DAFQLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTCDVWVFWVWNHTEVTIP  
YLATDVTVCVGPGAHKGQSVISLDLYTCELDLTNLILFSLSSISVSLFLMVMMTASHLYFWDVW  
YIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPVTEWVLAELVAKLEDPREKHFNLCLEE  
RDWLPGPVLENLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVILIFLE  
KPFQKSKFLQLRKRLCGSSVLEWPTNPQAHFYFWQCLKNALATDNHVAYSQVFKETV

**FIGURE 210A**

GGGTACCATTTCTGCGCTGCTGCAAGTTACGGAATGAAAAATTAGAACAACAGAAACATGGAA  
AACATGTTTCCTTCAGTCGTCAATGCTGACCTGCATTTTCTGCTAATATCTGGTTTCCTGTGA  
GTTATGCGCCGAAGAAAATTTTCTAGAAGCTATCCTTGTGATGAGAAAAAGCAAAATGACT  
CAGTTATTGCAGAGTGCAGCAATCGTCGACTACAGGAAGTTCCCCAAACGGTGGGCAAATAT  
GTGACAGAACTAGACCTGTCTGATAATTTTCATCACACACATAACGAATGAATCATTTCAAGG  
GCTGCAAAATCTCACTAAAATAAATCTAAACCACAACCCCAATGTACAGCACCAGAACGGAA  
ATCCCGGTATACAATCAAATGGCTTGAATATCACAGACGGGGCATTCCTCAACCTAAAAAAC  
CTAAGGGAGTTACTGCTTGAAGACAACCAGTTACCCCAATAACCTCTGGTTTGCCAGAGTC  
TTTGACAGAACTTAGTCTAATTCAAAACAATATATACAACATAACTAAAGAGGGCATTTCAA  
GACTTATAAACTTGAAAAATCTCTATTTGGCCTGGAAGTCTATTTTAAACAAAGTTTGCGAG  
AAAATAACATAGAAGATGGAGTATTTGAAACGCTGACAAATTTGGAGTTGCTATCACTATC  
TTTCAATTCTCTTTTACACGTCGCCACCCAACTGCCAAGCTCCCTACGCAAACCTTTTTCTGA  
GCAACACCCAGATCAAATACATTAGTGAAGAAGATTTCAAGGGATTGATAAATTTAACATTA  
CTAGATTTAAGCGGGAAGTGTCCGAGGTGCTTCAATGCCCCATTTCCATGCGTGCCTTGTGA  
TGGTGGTGCTTCAATTAATATAGATCGTTTTGCTTTTCAAACTTGACCCAACTTCGATACC  
TAAACCTCTCTAGCACTTCCCTCAGGAAGATTAATGCTGCCTGGTTTAAAAATATGCCTCAT  
CTGAAGGTGCTGGATCTTGAATTCAACTATTTAGTGGGAGAAATAGTCTCTGGGGCATTTTT  
AACGATGCTGCCCCGCTTAGAAATACTTGACTTGTCTTTTAACTATATAAAGGGGAGTTATC  
CACAGCATATTAATATTTCCAGAACTTCTCTAACTTTTGTCTCTACGGGCATTGCATTTA  
AGAGGTTATGTGTTCCAGGAAGTCAAGAGAAGATGATTTCCAGCCCCTGATGCAGCTTCCAAA  
CTTATCGACTATCAACTTGGGTATTAATTTTATTAAGCAAATCGATTTCAAACCTTTTCCAAA  
ATTTCTCCAATCTGGAAATTAATTTACTTGTGCAAAAACAGAATATCACCGTTGGTAAAAGAT  
ACCCGGCAGAGTTATGCAAATAGTTCTCTTTTCAACGTCATATCCGGAAACGACGCTCAAC  
AGATTTTGAGTTTGACCCACATTCGAACCTTTTATCATTTTCAACCGTCCTTTAATAAGCCAC  
AATGTGCTGCTTATGGAAAAGCCTTAGATTTAAGCCTCAACAGTATTTTCTTCATTGGGCCA  
AACCAATTTGAAAATCTTCTGACATTGCCTGTTTAAATCTGTCTGCAAATAGCAATGCTCA  
AGTGTTAAGTGGAAGTGAATTTTCAGCCATTCTCATGTCAAATATTTGGATTTGACAAACA  
ATAGACTAGACTTTGATAATGCTAGTGCTCTTACTGAATTTGTCCGACTTGGAAGTTCTAGAT  
CTCAGCTATAATTCACACTATTTTCAGAATAGCAGGCGTAACACATCATCTAGAATTTATTCA  
AAATTTCACAAATCTAAAAGTTTTAACTTGAGCCACAACAACATTTATACTTTAACAGATA  
AGTATAACCTGGAAAGCAAGTCCCTGGTAGAATTAGTTTTTCAGTGGCAATCGCCTTGACATT  
TTGTGGAATGATGATGACAACAGGTATATCTCCATTTTCAAAGGTCTCAAGAATCTGACACG  
TCTGGATTTATCCCTTAATAGGCTGAAGCACATCCCAAATGAAGCATTCCTTAATTTGCCAG  
CGAGTCTCACTGAACTACATATAAATGATAATATGTTAAAGTTTTTTAACTGGACATTACTC  
CAGCAGTTTCCCTCGTCTCGAGTTGCTTGACTTACGTGGAAACAACTACTCTTTTTTAACTGA  
TAGCCTATCTGACTTTACATCTTCCCTTCGGACACTGCTGCTGAGTCATAACAGGATTTCCC  
ACCTACCCTCTGGCTTTCTTTCTGAAGTCAGTAGTCTGAAGCACCTCGATTTAAGTTCCAAT  
CTGCTAAAAACAATCAACAAATCCGCACTTGAACTAAGACCACCACCAAATTTATCTATGTT  
GGAATACACGGAAACCCCTTTGAATGCACCTGTGACATTGGAGATTTCCGAAGATGGATGG  
ATGAACATCTGAATGTCAAATTTCCAGACTGGTAGATGTCAATTTGTGCCAGTCCTGGGGAT  
CAAAGAGGGAAGAGTATTTGTGAGTCTGGAGCTAACAACCTTGTGTTTCAGATGTCAGTGCAGT  
GATATTATTTTTCTTCACGTTCTTTATCACCAACCATGGTTATGTTGGCTGCCCTGGCTCACC  
ATTTGTTTTACTGGGATGTTTGGTTTATATATAATGTGTGTTTAGCTAAGGTAAAAGGCTAC  
AGGTCTCTTTCCACATCCCAAACCTTTCTATGATGCTTACATTTCTTATGACACCAAAGATGC  
CTCTGTTACTGACTGGGTGATAAATGAGCTGCGCTACCACCTTGAAGAGAGCCGAGACAAAA  
ACGTTCTCCTTTGTCTAGAGGAGAGGGATTGGGACCCGGGATTGGCCATCATCGACAACCTC  
ATGCAGAGCATCAACCAAAGCAAGAAAACAGTATTTGTTTTAACCAAAAAATATGCAAAAAG  
CTGGAACCTTTAAAACAGCTTTTTACTTGGCTTTGCAGAGGCTAATGGATGAGAACATGGATG  
TGATTATATTTATCCTGCTGGAGCCAGTGTTACAGCATTCTCAGTATTTGAGGCTACGGCAG  
CGGATCTGTAAGAGCTCCATCCTCCAGTGGCCTGACAACCCGAAGGCAGAAGGCTTGTTTTG  
GCAAACCTCTGAGAAATGTGGTCTTGACTGAAAATGATTCACGGTATAACAATATGTATGTG  
ATTCCATTAAGCAATACTAACTGACGTTAAGTCATGATTTTCGCGCCATAATAAAGATGCAAA  
GGAATGACATTTCTGTATTAGTTATCTATTGCTATGTAACAAATTATCCCAAACCTTAGTGG  
TTTAAAACAACACATTTGCTGGCCACAGTTTTTTGAGGGTCAGGAGTCCAGGCCCAGCATAA

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**FIGURE 210B**

CTGGGTCCTCTGCTCAGGGTGTCTCAGAGGCTGCAATGTAGGTGTTTACCAGAGACATAGGC  
ATCACTGGGGTCACACTCATGTGGTTGTTTTCTGGATTCAATTCCTCCTGGGCTATTGGCCA  
AAGGCTATACTCATGTAAGCCATGCGAGCCTCTCCCACAAGGCAGCTTGCTTCATCAGAGCT  
AGCAAAAAAGAGAGGTTGCTAGCAAGATGAAGTCACAATCTTTTGTAATCGAATCAAAAAAG  
TGATATCTCATCACTTTGGCCATATTCTATTTGTTAGAAGTAAACCACAGGTCCCACCAGCT  
CCATGGGAGTGACCACCTCAGTCCAGGGAAAACAGCTGAAGACCAAGATGGTGAGCTCTGAT  
TGCTTCAGTTGGTCATCAACTATTTCCCTTGACTGCTGTCCTGGGATGGCCTGCTATCTTG  
ATGATAGATTGTGAATATCAGGAGGCAGGGATCACTGTGGACCATCTTAGCAGTTGACCTAA  
CACATCTTCTTTTCAATATCTAAGAACTTTTGCCACTGTGACTAATGGTCCTAATATTAAGC  
TGTTGTTTATATTTATCATATATCTATGGCTACATGGTTATATTATGCTGTGGTTGCGTTCCG  
GTTTTATTTACAGTTGCTTTTACAAATATTTGCTGTAAACATTTGACTTCTAAGGTTTAGATG  
CCATTTAAGAACTGAGATGGATAGCTTTTAAAGCATCTTTTACTTCTTACCATTTTTTAAAA  
GTATGCAGCTAAATTCGAAGCTTTTGGTCTATATTGTTAATTGCCATTGCTGTAAATCTTAA  
AATGAATGAATAAAAATGTTTCATTTTACAAAAA

**FIGURE 211**

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSPCDEKKQNDVIAECSNRRLQEVPTVG  
KYVTELDLSDNFITHITNESFQGLQNLTKINLNHNPNVQHONGNPGIQSNGLNITDGAFLNL  
KNLRELLLEDNQLPQIPSGLPESLTELS LIQNNIYNITKEGISRLINLKNLYLAWNCYFNKV  
CEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKLFLSNTQIKYISEEDFKGLINL  
TLLDLSGNCPRCFNAPFPCVPCDGGASINIDRFAFQNL TQLRYLNLSSTSLRKINA AWFKNM  
PHLKVLDLEFNVLVGEIVSGAFLTMLPRLEILDLSFNYIKGSYPQHINISRNF SKLLSLRAL  
HLRGYVFQELREDDFQPLMQLPNLSTINLGINFIKQIDFKLFQNF SNLEIIYLS ENRISPLV  
KDTRQSYANSSSFQRHIRKRRSTDFEFDPHSNFYHFTRPLIKPQCAAYGKALDLSLNSIFFI  
GPNQFENLPDIACLNLSANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELS DLEV  
LDLSYN SHYFRIAGVTHHLEFIQNF TNLKVLNLSHNNIYT LT DKYNLESKSLVELVFSGNRL  
DILWNDDDNRYISIFKGLKNLTRLDLSLNRLKHIPNEAFLNLPASLT ELHINDNMLKFFNWT  
LLQQFPRLELLDLRGNKLLFLTDSLSDFTSSLRTLLLSHNRI SHLPSGFLSEVSSLKHLDLS  
SNLLKTINKSALETKTTTKLSMLELHGNPFECTCDIGDFRRWMDEHLNVKIPRLVDVICASP  
GDQRGKSIVSLELTTCVSDVTAVILFFFTFFITTMVMLAALAHHLFYWDVWFIYNVCLAKVK  
GYRSLSTSQT FYDAYISYDTKDASVTDWVINELRYHLEESRDKNVLLCLEERDWD PGLAIID  
NLMQSINQSKKTVFVLTKKYAKSWNFKTA FYLALQRLMDENMDV IIFILLEPVLQHSQYLRL  
RQRICKSSILQWPDNPKAEGLEFWQTLRNVVLTENDSRYNMYVDSIKQY

**FIGURE 212**

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCT  
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA  
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC  
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC  
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGA  
GCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAA  
GGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTT  
CTGGTGTTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGT  
CCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCCTCA  
CCACCTGCGACGGGACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGC  
CGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGAC  
CAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGA  
GCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCA  
GATGTGGATGAATGCAGTGCTAGGAGGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGCCGG  
CAGTTACTGGTGCCAGTGTTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGC  
CCAAGGGAGGGCCCCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAA  
GAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGC  
CCCCTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCC  
TGGTGCACCTCCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTCTCTG  
GAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGACTCGTGAAGTGGCCAGCGCCCCAGGCTG  
GACTGAGCCCCCTCACGCCGCCCTGCAGCCCCCATGCCCTGCCAACATGCTGGGGGTCCAG  
AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCTCCTCCCC  
TTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCAC  
CCCTGGCTACCCCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTG  
AGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAG  
GCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACATAAAAATGAAACGTGA  
AAGGGCGGCCGCGACTCTAGAGT  
CGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAAT

**FIGURE 213**

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSL SADGTLCV PKGGP P R V A  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKKDS

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**FIGURE 214**

GCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAG  
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCC  
AGCAGCATCAGAGCAGCCCCCTGTGGTTGGCAGCAAAGTTTCAGCTTGGCTGGGCCCCGCTGTGA  
GGGGCTTCGCGCTACGCCCTGCGGTGTCCCGAGGGGCTGAGGTCTCCTCATCTTCTCCCTAGC  
AGTGGATGAGCAACCCAACGGGGGGCCCCGGGAGGGGAACTGGCCCCGAGGGAGAGGAACCCC  
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCCAGGACCGGGGAGG  
CACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTC  
TCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGC  
TCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTA  
CCGGCCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTCCG  
TGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTAC  
CGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTA  
CGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATAT  
GCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCA  
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGGGGCGGCTG  
TCCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTGGGAGGGGGCACAGCC  
TGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCG  
ACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCT  
GGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGC  
ATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCCTTCCAGCAGCTCGGCCGCATCGAC  
TCCCTGAGCGAGCAGATTTCCTTCCTGGAGGAGCAGCTGGGGTCCTGCTCCTGCAAGAAAGA  
CTCGTGACTGCCCAGCGCTCCAGGCTGGACTGAGCCCCCTCACGCCGCCCTGCAGCCCCCATG  
CCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC  
AGGGCCTTCCTCCTCTTCCTCCTCCCCCTTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGAT  
GGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACCCCCACCCTGGCTACCCCAACGGCA  
TCCCAAGGCCAGGTGGACCCTCAGCTGAGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGAC  
CCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGAC  
CCCCAGCACAATAAAAATGAAACGTG

**FIGURE 215**

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDLSEQISFLEEQLGSCSCKKDS

**FIGURE 216**

CCCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA  
GGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAGGGCTAGGG  
TCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCCAGCAGCAT  
CAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGC  
CCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGC  
CTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGC  
AGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACG  
GGGACCCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGAC  
GGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGG  
GCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTC  
CTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAG  
CCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGA  
ATGCAGTGCTAGGAGGGGGCGGCTGTCCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT  
GCCAGTGTTGGGAGGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGG  
CCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAG  
GCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACA  
GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCC  
TTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTCCTGGAGGAGCAGCT  
GGGGTCCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGGCTGGACTGAGCCCC  
TCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCG  
GGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCCTCCTCCCCTTCCTCGGGAG  
GCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACC  
CCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTGAGGGAAGGTAC  
GAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGG  
CCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAATAAAAATGAAACGTG



**FIGURE 217**

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDVSESFVQRVYQPFLLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSL SADGTLCVPGGGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKKDS

**FIGURE 218**

GGTTGCCACAGCTGGTTTAGGGCCCCGACCACTGGGGCCCCCTTGTCAGGAGGAGACAGCCTC  
CCGGCCCCGGGGAGGACAAGTCGCTGCCACCTTTGGCTGCCGACGTGATTCCCTGGGACGGTC  
CGTTTCCTGCCGTCAGCTGCCGGCCGAGTTGGGTCTCCGTGTTTCAGGCCGGCTCCCCCTTC  
CTGGTCTCCCTTCTCCCGCTGGGCCGGTTTATCGGGAGGAGATTGTCTTCCAGGGCTAGCAA  
TTGGACTTTTGATGATGTTTGACCCAGCGGCAGGAATAGCAGGCAACGTGATTTCAAAGCTG  
GGCTCAGCCTCTGTTTCTTCTCTCGTGTAATCGCAAAACCCATTTTGGAGCAGGAATTCCAA  
TCATGTCCTGTGATGGTGGTGAGAAAGAAGGTGACACGGAAATGGGAGAAACTCCCAGGCAGG  
AACACCTTTTGCTGTGATGGCCGCGTCATGATGGCCCCGGCAAAAGGGCATTTTCTACCTGAC  
CCTTTTCCTCATCCTGGGGACATGTACACTCTTCTTCGCCTTTGAGTGCCGCTACCTGGCTG  
TTCAGCTGTCTCCTGCCATCCCTGTATTTGCTGCCATGCTCTTCCCTTTTCTCCATGGCTACA  
CTGTTGAGGACCAGCTTCAGTGACCCTGGAGTGATTCCTCGGGCGCTACCAGATGAAGCAGC  
TTTCATAGAAATGGAGATAGAAGCTACCAATGGTGCGGTGCCCCAGGGCCAGCGACCACCGC  
CTCGTATCAAGAATTTCCAGATAAACAACCAGATTGTGAAACTGAAATACTGTTACACATGC  
AAGATCTTCCGGCCTCCCCGGGCCTCCCATTTGCAGCATCTGTGACAACTGTGTGGAGCGCTT  
CGACCATCACTGCCCCCTGGGTGGGGAATTGTGTTGGAAAGAGGAACTACCGCTACTTCTACC  
TCTTCATCCTTTCTCTCTCCCTCCTCACAATCTATGTCTTCGCCTTCAACATCGTCTATGTG  
GCCCTCAAATCTTTGAAAATTGGCTTCTTGGAGACATTGAAAGAAACTCCTGGAAGTGTCT  
AGAAGTCCTCATTTGCTTCTTTACACTCTGGTCCGTCTGGGACTGACTGGATTTTCACTACTT  
TCCTCGTGGCTCTCAACCAGACAACCAATGAAGACATCAAAGGATCATGGACAGGGGAAGAAT  
CGCGTCCAGAATCCCTACAGCCATGGCAATATTGTGAAGAACTGCTGTGAAGTGCTGTGTGG  
CCCCTTGCCCCCAGTGTGCTGGATCGAAGGGGTATTTTGCCACTGGAGGAAAGTGGAAGTC  
GACCTCCCAGTACTCAAGAGACCAGTAGCAGCCTCTTGCCACAGAGCCCAGCCCCACAGAA  
CACCTGAACTCAAATGAGATGCCGGAGGACAGCAGCACTCCCGAAGAGATGCCACCTCCAGA  
GCCCCCAGAGCCACCACAGGAGGCAGCTGAAGCTGAGAAGTAGCCTATCTATGGAAGAGACT  
TTTGTGTTGTGTTTAAATTAGGGCTATGAGAGATTTAGGTGAGAAGTTAAACCTGAGACAGAG  
AGCAAGTAAGCTGTCCCTTTTAACTGTTTTTCTTTGGTCTTTAGTCACCCAGTTGCACACTG  
GCATTTTCTTGCTGCAAGCTTTTTTAAATTTCTGAACTCAAGGCAGTGGCAGAAGATGTCAG  
TCACCTCTGATAACTGGAAAAATGGGTCTCTTGGGCCCTGGCACTGGTTCTCCATGGCCTCA  
GCCACAGGGTCCCCTTGACCCCCCTCTCTTCCCTCCAGATCCCAGCCCCCTGCTTGGGGTC  
ACTGGTCTCATTCTGGGGCTAAAAGTTTTTGAGACTGGCTCAAATCCTCCCAAGCTGCTGCA  
CGTGCTGAGTCCAGAGGCAGTCACAGAGACCTCTGGCCAGGGGATCCTAACTGGGTCTTGG  
GGTCTTCAGGACTGAAGAGGAGGGAGAGTGGGGTCAGAAGATTCTCCTGGCCACCAAGTGCC  
AGCATTGCCCACAAATCCTTTTAGGAATGGGACAGGTACCTTCCACTTGTTGTANNNNNNNN  
NNNNNNNNNNNNNNNNNNNNNTTGTTTTTCTTTTGACTCCTGCTCCCATTAGGAGCAGGAATG  
GCAGTAATAAAAGTCTGCACCTTTGGTCATTTCTTTTCTCAGAGGAAGCCCGAGTGCTCACT  
TAAACACTATCCCCTCAGACTCCCTGTGTGAGGCCTGCAGAGGCCCTGAATGCACAAATGGG  
AAACCAAGGCACAGAGAGGCTCTCCTCTCCTCTCCTCTCCCCGATGTACCCTCAAAAAAAA  
AAAAATGCTAACCAGTTCTTCCATTAAGCCTCGGCTGAGTGAGGGAAAGCCCAGCACTGCTG  
CCCTCTCGGGTAACTCACCTAAGGCCTCGGCCACCTCTGGCTATGGTAACCACACTGGGG  
GCTTCCTCCAAGCCCCGCTCTTCCAGCACTTCCACCGGCAGAGTCCCAGAGCCACTTCACCC  
TGGGGGTGGGCTGTGGCCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTTTCAGGGAAGAAG  
ATTTATGTATTATATGTGGCTATATTTCTAGAGCACCTGTGTTTTCTCTTTCTAAGCCAG  
GGTCTGTCTGGATGACTTATGCGGTGGGGGAGTGTAACCGGAACTTTTCTATCTATTGAA  
GGCGATTAACTGTGTCTAATGCA

**FIGURE 219**

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGFYLTFLILGTCTLFFAFECRYLAV.  
QLSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP  
RIKNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHCPWVGNCVGKRNYRYFYL  
FILSLSLTIYVFAFNIVYVALKSLKIGFLETLKETPGTVLEVLCFFTLWSVVGLTGFHTF  
LVALNQT TNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVLCGPLPPSVLDRRGILPLEESGSR  
PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPPEPPEPPQEAAEA EK

**FIGURE 220**

AAAACCCTGTATTTTTTACAATGCAAATAGACAATNANCCTGGAGGTCTTTGAATTAGGTAT  
TATAGGGATGGTGGGGTTGATTTTTNTTCCTGGAGGCTTTTGGCTTTGGACTCTCNCTTTCT  
CCCACAGAGCNCTTCGACCATCACTGCCCCCTGGGTGGGGAATTGTGTTGGAAAGAGGAACTA  
CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCCNCTCACAATCTATGTCTTCGCCTTCA  
ACATCGT

**FIGURE 221**

GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA  
TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAGA  
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC  
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC  
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATT  
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA  
CAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCG  
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC  
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTTGTAGAGATTTT  
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC  
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGAC  
GAATACTTGGAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC  
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACCTATCCACCATA  
TTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC  
TCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA  
GAAAGGGGTGAAAGTGGAAAACAGACCTTTCTCTCAAACTCATCTTCTTCAATGTCTCTG  
AACATGACTATGGGAACTACACTTGCCTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC  
ATCATGCTATTTGGTCCAGGCGCCGTGAGCGAGGTGAGCAACGGCACGTGAGGAGGGCAGG  
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGAATGTGAGTGCC  
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACAC  
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA  
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAA  
AATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC  
ACACCCGGCTTGGAACCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA  
GGGCTCAGCCTCTCTGCCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA  
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG  
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA  
AAAAA

**FIGURE 222**

MKTIQPKMHNSISWAI FTGLAALCLFQGV PVRSGDATFPKAMD NVTVRQGESATLRCTIDNR  
VTRVAWLNRSTILYAGNDKWCLDPRV VLLSNTQTQYSIEIQNV DVYDEGPYTCSVQTDNHPK  
TSRVHLIVQVSPKIVEISSDISINEGNNISLT CIATGRPEPTVTWRHISPKAVGFVSEDEYL  
EIQGITREQSGDYEC SASNDVAAPVRRVKVTVNYPPISEAKGTGVPVGOKGTLQCEASAV  
PSAEFQWKDDKRLIEGKKG VKVENRPF LSKLIFFNVSEHDYGN YTCVASNKLGH TNASIML  
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLL LKF

**FIGURE 223**

GAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC  
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTT  
CCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTA  
TTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAAT  
GACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT  
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA  
ACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTGTAGAGATT  
TCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG  
ACCAGAG



**FIGURE 224**

ATGGCTGGTGACGGCGGGGCCGGGCAGGGGACCGGGGCCGGGCCCGGGAGCGGGCCAGCTG  
CCGGGAGCCCTGAATCACCGCCTGGCCCGACTCCACCATGAACGTCGCGCTGCAGGAGCTGG  
GAGCTGGCAGCAACGTGGGATTCCAGAAGGGGACAAGACAGCTGTTAGGCTCACGCACGCAG  
CTGGAGCTGGTCTTAGCAGGTGCCTCTCTACTGCTGGCTGCACTGCTTCTGGGCTGCCTTGT  
GGCCCTAGGGGTCCAGTACCACAGAGACCCATCCACAGCACCTGCCTTACAGAGGCCTGCA  
TTCGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCCCTGTGAGGACTTT  
TACCAGTTCTCCTGTGGGGGCTGGATTCCGGAGGAACCCCTGCCCGATGGGCGTTCTCGCTG  
GAACACCTTCAACAGCCTCTGGGACCAAAACCAGGCCATACTGAAGCACCTGCTTGAAAACA  
CCACCTTCAACTCCAGCAGTGAAGCTGAGCAGAAGACACAGCGCTTCTACCTATCTTGCCTA  
CAGGTGGAGCGCATTGAGGAGCTGGGAGCCCAGCCACTGAGAGACCTCATTGAGAAGATTGG  
TGGTTGGAACATTACGGGGGCCCTGGGACCAGGACAACCTTATGGAGGTGTTGAAGGCAGTAG  
CAGGGACCTACAGGGGCCACCCCATTTCTTACCGTCTACATCAGTGCCGACTCTAAGAGTTCC  
AACAGCAATGTTATCCAGGTGGACCAGTCTGGGCTCTTTCTGCCCTCTCGGGATTACTACTT  
AAACAGAACTGCCAATGAGAAAGTGCTCACTGCCTATCTGGATTACATGGAGGAACTGGGGA  
TGCTGCTGGGTGGGCGGCCACCTCCACGAGGGAGCAGATGCAGCAGGTGCTGGAGTTGGAG  
ATACAGCTGGCCAACATCACAGTGCCCCAGGACCAGCGGCGCGACGAGGAGAAGATCTACCA  
CAAGATGAGCATTTCGGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTCCTGT  
CTTTCTTGCTGTCACCATTTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGAT  
TATTTGCAGCAGGTGTCAGAGCTCATCAACCGCACGGAACCAAGCATCCTGAACAATTACCT  
GATCTGGAACCTGGTGCAAAAGACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAG  
AGAAGCTGCTGGAGACCCTCTATGGCACTAAGAAGTCCTGTGTGCCGAGGTGGCAGACCTGC  
ATCTCCAACACGGATGACGCCCTTGGCTTTGCTTTGGGGTCACTCTTCGTGAAGGCCACGTT  
TGACCGGCAAAGCAAAGAAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCATTTGAGG  
AGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCCGCCAGGCAGCCAAGGAGAAAGCA  
GATGCCATCTATGATATGATTGGTTTCCCAGACTTTATCCTGGAGCCCAAAGAGCTGGATGA  
TGTTTATGACGGGTACGAAATTTCTGAAGATTCTTTCTTCCAAAACATGTTGAATTTGTACA  
ACTTCTCTGCCAAGGTTATGGCTGACCAGCTCCGCAAGCCTCCAGCCGAGACCAGTGGAGC  
ATGACCCCCCAGACAGTGAATGCCTACTACCTTCCAACATAAGAATGAGATCGTCTTCCCCGC  
TGGCATCCTGCAGGCCCCCTTCTATGCCCGCAACCACCCCAAGGCCCTGAACTTCGGTGGCA  
TCGGTGTGGTCATGGGCCATGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGAC  
AAAGAAGGGAACCTGCGGCCCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCACAC  
GGCCTGCATGGAGGAACAGTACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCC  
AGACGCTGGGGGAGAACATTACTGACAACGGGGGGCTGAAGGCTGCCTACAATGCTTACAAA  
GCATGGCTGAGAAAGCATGGGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACCAACCACCA  
GCTCTTCTTCGTGGGATTTGCCCGAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCAG  
AGGGGCTGGTGACCGACCCCCACAGCCCTGCCCGCTTCCGCGTGCTGGGCACTCTCTCCAAC  
TCCCGTGACTTCCTGCGGCACTTCGGCTGCCCTGTGCGCTCCCCCATGAACCCAGGGCAGCT  
GTGTGAGGTGTGGTAGACCTGGATCAGGGGAGAAATGGCCAGCTGTCACCAGACCTGGGGCA  
GCTCTCCTGACAAAGCTGTTTGCTCTTGGGTGGGAGGAAGCAAATGCAAGCTGGGCTGGGT  
CTAGTCCCTCCCCCCCACAGGTGACATGAGTACAGACCTCCTCAATCACCACATTGTGCCT  
CTGCTTTGGGGGTGCCCTGCCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTTCCGT  
GTCACCCTGCCTGGAAGAGGTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCC

**FIGURE 225**

MNVALQELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSH  
STCLTEACIRVAGKILES LDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNOA  
ILKHLLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGGWNITGPWDQDN  
FMEVLKAVAGTYRATPFFT VYISADSKSSNSNVIQVDQSGFLPSRDYYLNRTANЕКVLTAY  
LDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRRDEEKIYHKMSISELQALAP  
SMDWLEFLSFLLSPLELSDSEPVVVYGMDYLQOVSELINRTEPSILNNYLIWNLVQKTTSSL  
DRRFESAQEKLLLETLYGTTKSCVPRWQTCISNTDDALGFALGSLEVKATFDROSKEIAEGMI  
SEIRTA FEEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISED SF  
FQNMLNLYNFS AKVMADQLRKPPSRDQWSMTPQTVNAYYLPTKNEIVFPAGILQAPFYARNH  
PKALNFGGIGVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQV  
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFAQVWCS  
VRTPESSHEGLVTDPHSPARFRVLGTLSNSRDFLRHFGCPVGSPMNP GQLCEVW

**FIGURE 226A**

GCCCCGGCCCTCCGCCCCCTCCGCACTCCCGCCTCCCTCCCTCCGCCCCGCTCCCGCGCCCTCCTC  
CCTCCCTCCTCCCCAGCTGTCCCGTTCGCGTCATGCCGAGCCTCCCGGCCCCGCGGCCCCCG  
CTGCTGCTCCTCGGGCTGCTGCTGCTCGGCTCCCGGCCCCGCGGCGCCGGCCCCAGAGCC  
CCCCGTGCTGCCCATCCGTTCCTGAGAAGGAGCCGCTGCCCGTTCGGGGAGCGGCAGGTAGGT  
GGGCGCCCCGGGGGAGGCGCGGGCGGGGAGTCGGGCTCGGGGCGAGTCAGCGCCAGCCCCGAG  
GGGGCGCGGGGGCGCAGGTGGCTCGGCGCGGGCGGGCGGCCCCGGAGGGTGGGCGGGGGCAGAAG  
GGCGCGGTGCCTGGGACCCGGGACCCGCGGGCAGCCCCCGGGGCGGCACACGGCGCGAGCTG  
GGCAGCGGCCCTCCAGCCAAGCCCGTCCCCGCAGGCTGCACCTTCGGCGGGAAGGTCTATGCC  
TTGGACGAGACGTGGCACC CGGACCTAGGGGAGCCATTCCGGGTGATGCGCTGCGTGCTGTG  
CGCCTGCGAGGCGCAGTGGGGTCGCCGTACCAGGGGCCCTGGCAGGGTCAGCTGCAAGAACA  
TCAAACCAGAGTGCCCAACCCCGGCCTGTGGGCAGCCGCGCCAGCTGCCGGGACACTGCTGC  
CAGACCTGCCCCCAGGACTTCGTGGCGCTGCTGACAGGGCCGAGGTGCGAGGCGGTGGCAGC  
AGCCCGAGTCTCGCTGCTGCGCTCTAGCCTCCGCTTCTCTATCTCCTACAGGCGGCTGGACC  
GCCCTACCAGGATCCGCTTCTCAGACTCCAATGGCAGTGTCTGTTTGAGCACCTGCAGCC  
CCCACCCAAGATGGCCTGGTCTGTGGGGTGTGGCGGGCAGTGCCCTCGGTTGTCTCTGCGGCT  
CCTTAGGGCAGAACAGCTGCATGTGGCACTTGTGACACTCACTCACCTTCAGGGGAGGTCT  
GGGGGCCCTCTCATCCGGCACCGGGGCCCTGTCCCCAGAGACCTTCAGTGCCATCCTGACTCTA  
GAAGGCCCCCACCAGCAGGGCGTAGGGGGCATCACCTGCTCACTCTCAGTGACACAGAGGA  
CTCCTTGCAATTTTTTGCTGCTCTTCCGAGGCCTTGCAAGACTAACCAGGTTCCCTTGAGGC  
TCCAGATTCTACACCAGGGGCAGCTACTGCGAGAACTTCAGGCCAATGTCTCAGCCCAGGAA  
CCAGGCTTTGCTGAGGTGCTGCCCAACCTGACAGTCCAGGAGATGGACTGGCTGGTGCTGGG  
GGAGCTGCAGATGGCCCTGGAGTGGGCAGGCAGGCCAGGGCTGCGCATCAGTGGACACATTG  
CTGCCAGGAAGAGCTGCGACGTCTTGCAAAGTGTCTTTGTGGGGCTAATGCCCTGATCCCA  
GTCCAAACGGGTGCTGCCGGCTCAGCCAGCCTCACTCTGCTAGGAAATGGCNCCCTGATCCT  
CCAGGTGCAATTGGTAGGGACAACCAGTGAGGTGGTGGCCATGACACTGGAAACCAAGCCTC  
AGCGGAGGGATCAGCCCCTGTCTGTGCCACATGGCTGGCCTATCCTCCCCCTGCCCCCAGG  
CCGTGGGTATCTGCCCTGGGCTGGGGTGCCCCAGGGGGCTCATATGCTGCTGCAGAAATGAGCT  
CTTCTGAACGTGGGCACCAAGGACTTCCCAGACGGAGAGCTTCGGGGGCAACGTGGCTGCC  
CTGCCCTACTGTGGGGCATAGCGCCCGCCCTGCCCGTGCCCTAGCAGGAGCCCTGGTGCTA  
CCCCCTGTGAAGAGCCAAGCAGCAGGGCACGCCCTGGCTTTCTTGGATACCCACTGTACCT  
GCACTATGAAGTGCTGCTGGCTGGGCTTGGTGGCTCAGAACAAAGGCACTGTCACTGCCACC  
TCCTTGGGCCTCCTGGAACGCCAGGGCCTCGGCGGCTGCTGAAGGGATTCTATGGCTCAGAG  
GCCCAGGGTGTGGTGAAGGACCTGGAGCCGGAAGTGTGCGGCACCTGGCAAAAGGCATGGC  
TTCCCTGATGATCACCACCAAGGTAGCCCCAGAGGGGAGCTCCGAGGGCAGCCTCTCCTCCC  
AGGTGCACATAGCCAACCAATGTGAGGTTGGCGGACTGCGCCTGGAGGCGGCGGGGGCCGAG  
GGGGTGCGGGCGCTGGGGGCTCCGGATACAGCCTCTGCTGCGCCGCTGTGGTGCCTGGTCT  
CCCGGCCCTAGCGCCCGCCAAACCTGGTGGTCTTGGGCGGCCCCGAGACCCCAACACATGCT  
TCTTCGAGGGGCGAGCAGCGCCCCACGGGGCTCGCTGGGCGCCCCAACTACGACCCGCTCTGC  
TCACTCTGCACCTGCCAGAGACGAACGGTGATCTGTGACCCGGTGGTGTGCCCACCGCCCAG  
CTGCCCCACACCCGGTGCAGGCTCCCGACCAGTGCTGCCCTGTTTGCCCTGGCTGCTATTTTG  
ATGGTGACCGGAGCTGGCGGGCAGCGGGTACGCGGTGGCACCCCGTTGTGCCCCCCTTTGGC  
TTAATTAAGTGTGCTGTCTGCACCTGCAAGCAGGGGGGCACTGGAGAGGTGCACTGTGAGAA  
GGTGCAGTGTCCCCGGCTGGCCTGTGCCAGCCTGTGCGTGTCAACCCACCGACTGCTGCA  
AACAGTGTCCAGGTGAGGCCACCCCCAGCTGGGGGACCCCATGCAGGCTGATGGGCCCCGG  
GGCTGCCGTTTTGCTGGGCAGTGGTTCCAGAGAGTCAGAGCTGGCACCCCTCAGTGCCCCC  
GTTTGGAGAGATGAGCTGTATCACCTGCAGATGTGGGGTAAGTGGGGAGCAGAGGCTTGTGT  
GAGGTGGGTACTGGGAGCCTGGTCTGGAGTAGGGAGACCTTCCCAGGGAGGTCCCTGAAGAA  
GCTGAAGGTCACTGTGTCCAGTGCCCTCTGGGGGACACTCAGTGTCTGCTCTGTCTTGTACC  
AGGCAGGGGTGCCTCACTGTGAGCGGGATGACTGTTCACTGCCACTGTCTGTGGCTCGGGG  
AAGGAGAGTCGATGCTGTTCCCGCTGCACGGGCCACCGGCGGCGTAAGTGAGGGAGTCCAGG  
GTCAGCAGCTGTGAGTGGAGGGCTCACCTGCCTGTGGGACTCCTGATCAGGGAAGGGAGCAC  
TCACTGTGTGCAGGAACAGTGCAGCCTGCCTCACAAGTGCCATTCCAATCCACCCTCACAGC  
AACCTGGTGAATTGTTATTTATGACCTTTTCTTTACAAATGAGATTTCTGAAGCTCAGAGA  
AATTAAGCAACGAGATGAAGGTACCCAGCTGTGTGCACTGACCTGTTTAGAAAATACTGGC

**FIGURE 226B**

CTTTCTGGGACCAAGGCAGGGATGCTTTGCCCTGCCCTCTATGCCTCTCTGTGCCTCTCCAC  
TCCCTCTCCCCTCCTCCAACATTCCCTCCCTTCTGTCTCCAGCAGCCCCAGAGACCAGAACT  
GATCCAGAGCTGGAGAAAGAAGCCGAAGGCTCTTAGGGAGCAGCCAGAGGGCCAAGTGACCA  
AGAGGATGGGGCCTGAGCTGGGGAAGGGGTGGCATCGAGGACCTTCTTGCATTCTCCTGTGG  
GAAGCCCAGTGCCTTTGCTCCTCTGTCTCCTGCCCTCTACTCCCACCCCCACTACCTCTGGGAAC  
CACAGCTCCACAAGGGGGGAGAGGCAGCTGGGCCAGACCGAGGTCACAGCCACTCCAAGTCCT  
GCCCTGCCACCCTCGGCCTCTGTCTGGAAGCCCCACCCCTTTCTTCCTGTACATAATGTCA  
CTGGCTTGTTGGGATTTTAAATTTATCTTCACTCAGCACCAAGGGCCCCGGACACTCCACTC  
CTGCTGCCCCCTGAGCTGAGCAGAGTCATTATTGGAGAGTTTTGTATTTATTAAAACATTTCT  
TTTTCAGTCTTTGGGCATGAGGTGGCTCTTTGTGGCCAGGAACCTGAGTGGGGCCTGGTGG  
AGAAGGGGCNGAGAGTAGGAGGTGAGAGAGAGGAGCTCTGACACTTGGGGAGCTGAAAGAGA  
CCTGGAGAGGCAGAGGATAGCGTGGC NNTTGGCTGGCATNCCTGGGTTCGCGAGAGGGGCTG  
GGGATGGTTCTTGAGATGGTCTAGAGACTCAAGAATTTAGGGAAGTAGAAGCAGGATTTTGA  
CTCAAGTTTAGTTTCCACATCGCTGGCCTGTTTGCTGACTTCATGTTTGAAGTTGCTCCAG  
AGAGAGAATCAAAGGTGTCACCAGCCCCCTCTCTCCCTCCTTCCCTTCCCTTCCCTTTCTTC  
CCTCCCCCTCCCCTCCCCTCCCCTCCCCTCC

**FIGURE 227**

GGCCGAGCGGGGGTGCTGCGCGGCGGCCGTGATGGCTGGTGACGGCGGGGCCGGGCAGGGGA  
CCGGGGCCGCGGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACCGCCTGGCCCCGAC  
TCCACCATGAACGTGCGGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG  
GACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC  
TGCTGGCTGCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCA  
TCCCACAGCACCTGCCTTACAGAGGCCTGCATTCGAGTGGCTGGAAAAATCCTGGAGTCCCT  
GGACCGAGGGGTGAGCCCCTGTGAGGACTTTTACCAGTTCTCCTGTGGGGGCTGGATTCCGA  
GGAACCCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAC  
CAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAGCA  
GAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC  
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAG  
GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCATTCTTCAC  
CGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGCAATGTTATCCAGGTGGACCAGTCTG  
GGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC  
ATCTTCCGAACCCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT  
TTGCCAAGGGTCAGAGCAGGGAAGGTGAGCCTATCCTGTCACCTAGTGAACAACTGCCCCCT  
CCTTTCTTTCTTCTTTTCTTCCCTCCCTCCCTTTCTTCCCCTTTTCTTCCCTTCCCTTCC  
TCTTATTCTTCTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTG  
GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTCAGTGTGATGGGTTCATGGACCT  
AGATAGGCTGATAACAAAGCTCACAAGAGGGTCCTGAGGATTCAGGAGAGACTTATGGAGCC  
AGCAAAGTCTTCTGAAGAGATTGCATTTGAGCCAGGTCCTGTAG



**FIGURE 228**

ATGCCTACTACCTTCCAAC TAAGAATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCCC  
TTCTATGCCCCGCAACCACCCCAAGGCCCTGAACTTCGGTGGCATCGGTGTGGTCATGGGCCA  
TGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTGCGGC  
CCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCACACGGCCTGCATGGAGGAACAG  
TACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT  
TGCTGACAACGGGGGGGCTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG  
GGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACCAACCACCAGCTCTTCTTCGTGGGATTT  
GCCCAGGTGTGGTGTCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGGGCTGGTGACCGACCC  
CCACAGCCCTGCCCGCTTCCGCGTGCTGGGCACTCTCTCCAACCTCCCGTGACTTCCTGCGGC  
ACTTCGGCTGCCCTGTCTGGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC  
TGGATCAGGGGAGAAATGGCCAGCTGTCACCAGACCTGGGGCAGCTCTCCTGACAAAGCTGT  
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TGGCCCTTATAGGACC